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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 09:06:05 ; Search time 544 Seconds
(without alignments)
9808.637 Million cell updates/sec

Title: US-09-373-658C-1

Perfect score: 3261

Sequence: 1 atggggaacgcggagcggc.....tgcatgtgtcatnagtctn 3261

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCRU COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3160	96.9	4676	3	US-09-130-491-1
2	3156.8	96.8	3899	4	US-09-568-559-1
3	3150.6	96.6	4858	3	US-09-392-184-1
4	2631.4	80.7	3706	3	US-09-484-9708-58
5	2131.6	65.4	2184	4	US-09-445-023A-2
6	1655	50.8	2184	4	US-09-445-023A-13
7	666.2	20.4	3638	3	US-09-369-364A-8
8	629.8	19.3	2853	4	US-10-009-332-2
9	603.4	18.5	4192	3	US-09-122-1268-1
10	603.4	18.5	4192	4	US-09-634-286A-1
11	603.4	18.5	4192	4	US-10-247-685-1
12	558.6	17.1	3250	3	US-09-122-1268-14
13	558.6	17.1	3250	4	US-09-634-286A-14
14	558.6	17.1	3250	4	US-10-247-685-14
15	544.2	16.7	3126	3	US-09-392-184-7
16	542.8	16.6	3002	3	US-09-369-364A-1
17	369.4	11.3	5804	3	US-09-369-364A-12
18	359.8	11.0	2623	3	US-09-369-364A-14
19	325	10.0	6659	4	US-09-321-987B-1
20	324	9.9	2114	3	US-09-130-491-7
21	268.6	8.2	739	3	US-09-369-364A-10
22	198.4	6.1	1520	3	US-09-369-364A-3
23	175.8	5.4	303	4	US-09-445-023A-14
24	145.6	4.5	703	3	US-09-392-184-6
25	141.8	4.3	3218	3	US-09-369-364A-6
26	140.2	4.3	5357	3	US-09-392-184-5
27	115.2	3.5	3571	4	US-09-799-451-411

28	113.6	3.5	3377	4	US-09-981-953A-3	Sequence 3, Appli
29	109.4	3.4	3675	3	US-09-930-872-3	Sequence 3, Appli
30	109.4	3.4	3675	4	US-10-217-774-3	Sequence 3, Appli
31	109.4	3.4	3766	4	US-09-981-953A-1	Sequence 1, Appli
32	109.4	3.4	4042	3	US-09-930-872-5	Sequence 5, Appli
33	109.4	3.4	4042	4	US-10-217-774-5	Sequence 5, Appli
34	104.8	3.2	3158	4	US-09-949-016-1988	Sequence 1988, Ap
35	102.8	3.2	2274	4	US-09-963-791-23	Sequence 23, Appli
36	102.8	3.2	2727	4	US-09-963-791-1	Sequence 1, Appli
37	96.6	3.0	1061	4	US-09-270-767-995	Sequence 995, App
38	96.6	3.0	1061	4	US-09-270-767-16277	Sequence 16277, A
39	84.6	2.6	1317	4	US-09-963-791-21	Sequence 21, Appli
40	84.6	2.6	1770	4	US-09-963-791-11	Sequence 11, Appli
41	84.4	2.6	3885	3	US-09-369-364A-16	Sequence 16, Appli
42	83	2.5	1071	4	US-09-963-791-19	Sequence 19, Appli
43	83	2.5	1524	4	US-09-963-791-9	Sequence 9, Appli
44	77.4	2.4	2799	4	US-09-181-339-2	Sequence 2, Appli
45	76	2.3	944	4	US-09-461-325-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-09-130-491-1

; Sequence 1, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 4676

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (460)...(3360)

US-09-130-491-1

Query Match 96.9%; Score 3160; DB 3; Length 4676;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3177; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY	1	ATGGGAAACGCGAGCGGGCTCGGGGTCTCGAGCTTTGGGCGCCGTCACCGCTCTG 60
DB	511	ATGGGAAACGCGAGCGGGCTCGGGGTCTCGAGCTTTGGGCGCCGTCACCGCTCTG 570
QY	61	CTGCTCGCGCGCGGCTACTGGCCGTCTCGAGCGCACTCGGCGCCCTCCGAGGAGAC 120
DB	571	CTGCTCGCGCGCGGCTACTGGCCGTCTCGAGCGCACTCGGCGCCCTCCGAGGAGAC 630
QY	121	GAGGAGCTAGTGTGTCGCGAGCTGGAGCGCCCGGGACACGCGGACACGCGCTCCGC 180
DB	631	GAGGAGCTAGTGTGTCGCGAGCTGGAGCGCCCGGGACACGCGGACACGCGCTCCGC 690
QY	181	CTGCACGCTTTCACGACGAGCTGAGATCTGAGCTCGGCGCCCGACACGAGCTTTTGGCG 240
DB	691	CTGCACGCTTTCACGACGAGCTGAGATCTGAGCTCGGCGCCCGACACGAGCTTTTGGCG 750
QY	241	CCCGGTTTACGCTCCAGACGTTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGAA 300
DB	751	CCCGGTTTACGCTCCAGACGTTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGAA 810

QY 301 ACCGACCTGGCGCACTGTTCTACTCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
DB |||||
DB 811 ACCGACCTGGCGCACTGTTCTACTCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 870
QY 361 GCCCTCAGCCTCTGGAGGCGGTGCGCGCGCTTCTACTCTGCTGGGGAGCGGTATTTTC 420
DB |||||
DB 871 GCCCTCAGCCTCTGGAGGCGGTGCGCGCGCTTCTACTCTGCTGGGGAGCGGTATTTTC 930
QY 421 ATCCAGCGCTGCCCGCGCGCAGGAGCGCTCGCCACCGCGCGCCCGCAGGGGAGAGCGG 480
DB |||||
DB 931 ATCCAGCGCTGCCCGCGCGCAGGAGCGCTCGCCACCGCGCGCCCGCAGGGGAGAGCGG 990
QY 481 CGGCAACCACTACAGTTCCACTCTCTGCGCGGGAATCGGAGGGGAGCTAGCGCGCACG 540
DB |||||
DB 991 CGGCAACCACTACAGTTCCACTCTCTGCGCGGGAATCGGAGGGGAGCTAGCGCGCACG 1050
QY 541 TCGCGGGTCTGTCGAGCAGACGAGCCCGCGCGCACTGGGAAAGCGGAGACCGAGACGAGGAC 600
DB |||||
DB 1051 TCGCGGGTCTGTCGAGCAGACGAGCCCGCGCGCACTGGGAAAGCGGAGACCGAGACGAGGAC 1110
QY 601 GAAGGACCTGAGGGCGAGGACGAGGGGCTCAGTGGTGGCGCAGGACCGCGCACTGCAA 660
DB |||||
DB 1111 GAAGGACCTGAGGGCGAGGACGAGGGGCTCAGTGGTGGCGCAGGACCGCGCACTGCAA 1170
QY 661 GCGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGAGCGATTTGTCCAGTCCAC 720
DB |||||
DB 1171 GCGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGAGCGATTTGTTCAGTCCAC 1230
QY 721 CGCTATGTGGAAACCACTGTTGTGGCAGACCACTGATGGCGAATTCACGGCAGTGGT 780
DB |||||
DB 1231 CGCTATGTGGAAACCACTGTTGTGGCAGACCACTGATGGCGAATTCACGGCAGTGGT 1290
QY 781 CTAAAGCAATTACTCTCAGTGTGTTTTCGGTGGCAGCGCAGATTGTACAAACACCCCGAC 840
DB |||||
DB 1291 CTAAAGCAATTACTCTCAGTGTGTTTTCGGTGGCAGCGCAGATTGTACAAACACCCCGAC 1350
QY 841 ATTCTGTAATTAGTTAGCTGCTGTTGTTGAAGATCTTGGTCACTCAGCATGAACAGAGA 900
DB |||||
DB 1351 ATTCTGTAATTAGTTAGCTGCTGTTGTTGAAGATCTTGGTCACTCAGCATGAACAGAGA 1410
QY 901 GGGCCGGAAGTGACCTCCAAATGCTCCCTCACTCTCGCGAATCTTTGCAACTGGCAGAG 960
DB |||||
DB 1411 GGGCCGGAAGTGACCTCCAAATGCTCCCTCACTCTCGCGAATCTTTGCAACTGGCAGAG 1470
QY 961 CAGCAACCCACCACTGACCGGATGACAGACACTATGACACAGCAATCTTTTCCAC 1020
DB |||||
DB 1471 CAGCAACCCACCACTGACCGGATGACAGACACTATGACACAGCAATCTTTTCCAC 1530
QY 1021 AGACAGGACTTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAAT 1080
DB |||||
DB 1531 AGACAGGACTTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAAT 1590
QY 1081 GTGTGTATCCGAGCAGAGCTGCTCGGTATAGAGATGATGGTTTCAAGCTGCCCTTC 1140
DB |||||
DB 1591 GTGTGTATCCGAGCAGAGCTGCTCGGTATAGAGATGATGGTTTCAAGCTGCCCTTC 1650
QY 1141 ACCACGCCCATGAAATAGGCCACGTGTTTACATGCCCATGATGATGCAAGCAGTGT 1200
DB |||||
DB 1651 ACCACGCCCATGAAATAGGCCACGTGTTTAACTATGCCCATGATGATGCAAGCAGTGT 1710
QY 1201 GCGAGCTTAAATGTTGTAACCCAGGATCCACATGATGGGCTCAATGCTTTCCAACTCG 1260
DB |||||
DB 1711 GCGAGCTTAAATGTTGTAACCCAGGATCCACATGATGGGCTCAATGCTTTCCAACTCG 1770
QY 1261 GACACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAATCATTTCTGGATAT 1320
DB |||||
DB 1771 GACACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAATCATTTCTGGATAT 1830
QY 1321 GGTATGGGGATGTTTGTATGACAGCTCAGATCCCATACAGCTCCAGCGCATCTC 1380
DB |||||
DB 1831 GGTATGGGGATGTTTGTATGACAGCTCAGATCCCATACAGCTCCAGCGCATCTC 1890
QY 1381 CCTGGCACCTCGTACGATGCCAACCGGACGTGCCAGTTTACATTTTGGGAGGACTCCAA 1440

DB 1891 CCTGGCACCTCGTACGATGCCAACCGGACGTGCCAGTTTACATTTGGGAGGACTCCAAA 1950
QY 1441 CACTGCCCTGATGACAGCAGCACATGTAGCACTTGTGGTGTACCGGCACCTCTCGTGGG 1500
DB 1951 CACTGCCCGATGACCGCAGCACATGTAGCACTTGTGGTGTACCGGCACCTCTCGTGGG 2010
QY 1501 GTGCTGGTGTCTAAACCAACACTTCCCGTGGGGGATGGCACCGACTGTGGAGAGGG 1560
DB |||||
DB 2011 GTGCTGGTGTCTAAACCAACACTTCCCGTGGGGGATGGCACCGACTGTGGAGAGGG 2070
QY 1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCAATTTTATACGCT 1620
DB |||||
DB 2071 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCAATTTTATACGCT 2130
QY 1621 TTTTCAATGAAGTGGGGAATGTGGGGCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680
DB |||||
DB 2131 TTTTCAATGAAGTGGGGAATGTGGGGCTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2190
QY 1681 GGAGTCCAGTACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAAGTAC 1740
DB |||||
DB 2191 GGAGTCCAGTACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAAGTAC 2250
QY 1741 TGTGAAGGCAAAACGAGTGGCTACAGATCTCTGTAACTTGTAGGACTGTCCAGACAATAAT 1800
DB |||||
DB 2251 TGTGAAGGCAAAACGAGTGGCTACAGATCTCTGTAACTTGTAGGACTGTCCAGACAATAAT 2310
QY 1801 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACAACAAGAGTTTCAAGAGTCTCTTT 1860
DB |||||
DB 2311 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACAACAAGAGTTTCAAGAGTCTCTTT 2370
QY 1861 GGGAGTGGGCTGCGGTGGAAATGGATCCCAAGTACGCTGGGCTCTACCAAGGACAGG 1920
DB |||||
DB 2371 GGGAGTGGGCTGCGGTGGAAATGGATCCCAAGTACGCTGGGCTCTACCAAGGACAGG 2430
QY 1921 TGCAGACTCATCTGCAAGCCAAAGGCAATGGCTACTCTTCTGGTTTTCAGCCCCAAGGTT 1980
DB |||||
DB 2431 TGCAGACTCATCTGCAAGCCAAAGGCAATGGCTACTCTTCTGGTTTTCAGCCCCAAGGTT 2490
QY 1981 GTAGATGTGTCTCCATGTAGCCAGATTCACACTCTGTCTGTGTGCAAGGACAGTGTGTA 2040
DB |||||
DB 2491 GTAGATGTGTCTCCATGTAGCCAGATTCACACTCTGTCTGTGTGCAAGGACAGTGTGTA 2550
QY 2041 AAAGCTGTGTGTATGTCGATCATAGACTCCAAAAGAAAGTTTGAATAATGTGGTGTTCG 2100
DB |||||
DB 2551 AAAGCTGTGTGTATGTCGATCATAGACTCCAAAAGAAAGTTTGAATAATGTGGTGTTCG 2610
QY 2101 GGGGAAATGGATCTACTTGTAAATAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2160
DB |||||
DB 2611 GGGGAAATGGATCTACTTGTAAATAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2670
QY 2161 TATCATGATATCATCACAATTCACACTGGAGCCCAACATCGAAAGTGAACAGCGGAAC 2220
DB |||||
DB 2671 TATCATGATATCATCACAATTCACACTGGAGCCCAACATCGAAAGTGAACAGCGGAAC 2730
QY 2221 CAGAGGGATCAGGAACAATGGCAGCTTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2280
DB |||||
DB 2731 CAGAGGGATCAGGAACAATGGCAGCTTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2790
QY 2281 ATTCTTAATGGTGTACTACATTTGTGCCCTTTAGAGGAAGACATTTATGTACAAAGTGT 2340
DB |||||
DB 2791 ATTCTTAATGGTGTACTACATTTGTGCCCTTTAGAGGAAGACATTTATGTACAAAGTGT 2850
QY 2341 GTCCTTGAGGTACAGCGCTCCTCTCGGGCATTTGGAAAGAAATTCGACGCTTTTAGCCCTCTC 2400
DB |||||
DB 2851 GTCCTTGAGGTACAGCGCTCCTCTCGGGCATTTGGAAAGAAATTCGACGCTTTTAGCCCTCTC 2910
QY 2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCCTTCGACCTAAAAATAAA 2460
DB |||||
DB 2911 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCCTTCGACCTAAAAATAAA 2970
QY 2461 TACACTTCTCGTAAAGAGGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520

2971 TACACCTACTCTGTAAGAAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 3030
2521 TGGGTCAATGAGAGTGGGCGAATCTTCTAAGTCATGTAATGTTGGTTGGCAGAGA 2580
3031 TGGGTCAATGAGAGTGGGCGAATCTTCTAAGTCATGTAATGTTGGTTGGCAGAGA 3090
2581 CTGGTAGAATGCCGAGACATTAATGACAGCCTGCTTCCAGTGTGCAAGGAAGTGAAG 2640
3091 CTGGTAGAATGCCGAGACATTAATGACAGCCTGCTTCCAGTGTGCAAGGAAGTGAAG 3150
2641 CAGCAGACACAGACTTGTGTGAGACCATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 2700
3151 CAGCAGACACAGACTTGTGTGAGACCATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 3210
2701 TCATCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
3211 TCATCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAAGAGCTTGAAGTGTCTGTCC 3270
2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTT 2820
3271 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTT 3330
2821 ATAGACTTTTGCACATGGCAGAAATGAGTTAAGTGTGTTAAGTGTGTTAGCTTTGA-G 2879
3331 ATAGACTTTTGCACATGGCAGAAATGAGTTAAGTGTGTTAAGTGTGTTAGCTTTGAGG 3390
2880 GCAGGCAAGTGCAGGAGGCTGTGTCAGGGAAGCAAGAGGCTGGAGGATCCAGCG 2939
3391 GCAGGCAAGTGCAGGAGGCTGTGTCAGGGAAGCAAGAGGCTGGAGGATCCAGCG 3450
2940 TATCTTCCAGTAAACAGTGCAGTGTATCATGTAAGTGGGATTTAGGGGTAGATAGAA 2999
3451 TATCTTCCAGTAAACAGTGCAGTGTATCATGTAAGTGGGATTTAGGGGTAGATAGAA 3510
3000 AGAGTTGAATCATCAGAGTAACATGCGCAGTTGCAATTTGATAGATAGTGTAGTGA 3059
3511 AGAGTTGAATCATCAGAGTAACATGCGCAGTTGCAATTTGATAGATAGTGTAGTGA 3570
3060 TTATTAACCTCTCAGCAGTATAGCATATAAANCCCCGGCATTTATTATTATTATT 3119
3571 TTATTAACCTCTCAGCAGTATAGCATATAAANCCCCGGCATTTATTATTATTATT 3630
3120 CTTTGTGTACATCTATTACAAAGTTTAGAAAAAACAAGCAATTTGTCAAAAAAAGAA 3179
3631 CTTTGTGTACATCTATTACAAAGTTTAGAAAAAACAAGCAATTTGTCAAAAAAAGT 3690
3180 AAAAAAAA 3188
3691 CTATTACAA 3699

RESULT 2

US-09-568-559-1

; Sequence 1, Application US/09568559

; Patent No. 6649377

; GENERAL INFORMATION:

; APPLICANT: Klonowski, Paul

; APPLICANT: Allard, John

; APPLICANT: Heller, Renu

; APPLICANT: Van Wart, Harold

; TITLE OF INVENTION: Human Aggreganase and Nucleic Acid

; FILE REFERENCE: ROCH-002

; CURRENT APPLICATION NUMBER: US/09/568,559

; CURRENT FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: 60/133,343

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3889

; TYPE: DNA

; ORGANISM: human

US-09-568-559-1

Query Match 96.8%; Score 3156.8; DB 4; Length 3889;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1 ATGGGAAACCGGAGCGGGCTCCGGGTTCTCGAGTCTTTGGGCCCTATCCACGCTGCTG 60
DB 59 ATGGGAAACCGGAGCGGGCTCCGGGTTCTCGAGTCTTTGGGCCCTATCCACGCTGCTG 118
QY 61 CTGCTCGCCGCGCGCTACTGCGCGTCTCGAGCCTCGGGCGCCCTCCGAGGAGGAC 120
DB 119 CTGCTCGCCGCGCGCTACTGCGCGTCTCGAGCCTCGGGCGCCCTCCGAGGAGGAC 178
QY 121 GAGGAGCTAGTGTGTGCGGAGCTGAGCGCGCCCGGGACACGGGACACGCGCTCCGC 180
DB 179 GAGGAGCTAGTGTGTGCGGAGCTGAGCGCGCCCGGGACACGGGACACGCGCTCCGC 238
QY 181 CTGCAAGCTTTGAACAGCAGCTGATCTGAGCTCGGGCCCGACAGCAGCTTTTGGCG 240
DB 239 CTGCAAGCTTTGAACAGCAGCTGATCTGAGCTCGGGCCCGACAGCAGCTTTTGGCG 298
QY 241 CCGGCTTCCAGCTCCAGAACGTTGGGGCGCAATCCGGGTCGAGACGCGCTTCCGAA 300
DB 299 CCGGCTTCCAGCTCCAGAACGTTGGGGCGCAATCCGGGTCGAGACGCGCTTCCGAA 358
QY 301 ACCGACTTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
DB 359 ACCGACTTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 418
QY 361 GCCTCAGCTCTGCGAGGGCGTGCAGGCGCTTCTACTCGCGCGCGCTTCTACTCGCGCGG 420
DB 419 GCCTCAGCTCTGCGAGGGCGTGCAGGCGCTTCTACTCGCGCGCGCTTCTACTCGCGCGG 478
QY 421 ATCCAGCGCTGCCCGCGCGCGAGCGCTCCGCCACCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 479 ATCCAGCGCTGCCCGCGCGCGAGCGCTCCGCCACCGCGCGCGCGCGCGCGCGCGCGCG 538
QY 481 CCGGCACTACTACAGTTCCACCTCTCTGCGCGGCAATCGGCGGCGCGCGCGCGCGCGCG 540
DB 539 CCGGCACTACTACAGTTCCACCTCTCTGCGCGGCAATCGGCGGCGCGCGCGCGCGCGCG 598
QY 541 TGGGGGTGTGGAACGACGAGCCCCCGCGCGCTTGGGAAAGCGAGACCGAAGAGCGAGAC 600
DB 599 TGGGGGTGTGGAACGACGAGCCCCCGCGCGCTTGGGAAAGCGAGACCGAAGAGCGAGAC 658
QY 601 GAAGGACCTGAGGCGCGAGGAGCGCTCAGTGTGCGCGAGGACCGCGCGCTGCA 660
DB 659 GAAGGACCTGAGGCGCGAGGAGCGCTCAGTGTGCGCGAGGACCGCGCGCTGCA 718
QY 661 GCGTAGGACAGCCCAAGGAACTGGAAGCATTAAGAAAGCGATTTGTGTCCAGTCAC 720
DB 719 GCGTAGGACAGCCCAAGGAACTGGAAGCATTAAGAAAGCGATTTGTGTCCAGTCAC 778
QY 721 CGCTATGTGGAACCAATGCTTGTGCGAGACCACTCGATGCGAGATTTCCAGCGAGTGGT 780
DB 779 CGCTATGTGGAACCAATGCTTGTGCGAGACCACTCGATGCGAGATTTCCAGCGAGTGGT 838
QY 781 CTAAAGCATTTACCTTCTCAGTTGTTTTCGGTGGCAGCGAGATTTGTAACAACACCCGAGC 840
DB 839 CTAAAGCATTTACCTTCTCAGTTGTTTTCGGTGGCAGCGAGATTTGTAACAACACCCGAGC 898
QY 841 ATTCTGAATTCAGTTAGCTTGGTGGTGGTGAAGATCTTGGTTCATCCAGTGAACAGAAG 900
DB 899 ATTCTGAATTCAGTTAGCTTGGTGGTGGTGAAGATCTTGGTTCATCCAGTGAACAGAAG 958
QY 901 GGGCGGAGTGAACCTTCAATGCTGCCCTCAGTCTGCGGAACTTTTGCACACTGCGAGAAG 960
DB 959 GGGCGGAGTGAACCTTCAATGCTGCCCTCAGTCTGCGGAACTTTTGCACACTGCGAGAAG 1018
QY 961 CAGCAACACCCAGTGAACCGGATGAGAGCCTATGACACAGCAATTTCTTTTCAAC 1020
DB 1019 CAGCAACACCCAGTGAACCGGATGAGAGCCTATGACACAGCAATTTCTTTTCAAC 1078

QY 1021 AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGATCGCTGATGTGGAACT 1080
DB AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGATCGCTGATGTGGAACT 1138
QY 1081 GTGTGTGATCCAGCAGAAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTCCCTTC 1140
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QY 1141 ACCACAGCCCATGAATTAGGCCACGTGTTTAAATGCGCACATGATGATGCAAAAGCAGTGT 1200
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DB GCCAGCCTTAATGCTGTAACACAGATTCGCCACATGATGGCGTCAATGCTTCCAACTCG 1318
QY 1261 GACCACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAACATATTTCTGGATAAT 1320
DB GACCACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAACATATTTCTGGATAAT 1378
QY 1321 GGTATGGGGATGTTGATGGAAGGCTCAGAAATCCATACAGCTCCAGGCGATCTC 1380
DB GGTATGGGGATGTTGATGGAAGGCTCAGAAATCCATACAGCTCCAGGCGATCTC 1438
QY 1381 CCTGGCACCCTGATGATGSCCAACCGGAGTCCAGTGTTCATATTTGGGGAGGACTCCAAA 1440
DB CCTGGCACCCTGATGATGSCCAACCGGAGTCCAGTGTTCATATTTGGGGAGGACTCCAAA 1498
QY 1441 CACTGCCCTGATGACCCAGCACATGTAGCACCTTGTGGTGATCCGGCACCTCTCGTGGG 1500
DB CACTGCCCTGATGACCCAGCACATGTAGCACCTTGTGGTGATCCGGCACCTCTCGTGGG 1558
QY 1501 GTGCTGTGTGTAACCAAACACTTCCGTGGGGGATGGACACAGCTGTGGAGAAGG 1560
DB GTGCTGTGTGTAACCAAACACTTCCGTGGGGGATGGACACAGCTGTGGAGAAGG 1618
QY 1561 AAATGCTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTCATACGCT 1620
DB AAATGCTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTCATACGCT 1678
QY 1621 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGAGACTGTTCGAGAACGTCGGTGGA 1680
DB TTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGAGACTGTTCGAGAACGTCGGTGGA 1738
QY 1681 GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCAAAGAAATGGAGGGAGTAC 1740
DB GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCAAAGAAATGGAGGGAGTAC 1798
QY 1741 TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTTGAGACTGTCCAGACAAATAT 1800
DB TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTTGAGACTGTCCAGACAAATAT 1858
QY 1801 GGAATAACCTTTAGAGAGGAACAATGTGAAGCACACAACAGTGTTCAAAAGCTTCCTTT 1860
DB GGAATAACCTTTAGAGAGGAACAATGTGAAGCACACAACAGTGTTCAAAAGCTTCCTTT 1918
QY 1861 GGGAGTGGCCCTCGGTGGAATGGATTCACAGTACGCTGGCGTCTCACCAAGGACAGG 1920
DB GGGAGTGGCCCTCGGTGGAATGGATTCACAGTACGCTGGCGTCTCACCAAGGACAGG 1978
QY 1921 TGCAGACTCATCTGCCAAGCCAAAGCAATGGCTACTTCTGTTTTCAGGCCCAAGGTT 1980
DB TGCAGACTCATCTGCCAAGCCAAAGCAATGGCTACTTCTGTTTTCAGGCCCAAGGTT 2038
QY 1981 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040
DB GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2098
QY 2041 AAAGCTGGTGTGATCGCATATAGACTCCAAAGAAAGTTCATAAATGTGGTGTTCG 2100
DB AAAGCTGGTGTGATCGCATATAGACTCCAAAGAAAGTTCATAAATGTGGTGTTCG 2158

QY 2101 GGGGAAATGGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160
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QY 2161 TATCATGATATCATCAAAATTCCAACTGGAGCCAACTGGAAGTGAACAGCGGAAC 2220
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QY 2221 CAGAGGGATCCAGGAACAATGGGAGCTTCTTGGCCATCAAGCTGCTGATGGCACATAT 2280
DB CAGAGGGATCCAGGAACAATGGGAGCTTCTTGGCCATCAAGCTGCTGATGGCACATAT 2338
QY 2281 ATTCTTAATGTGACTACACTTTTGTCCACTTTAGAGCAAGACATTTATGTACAAAGTGT 2340
DB ATTCTTAATGTGACTACACTTTTGTCCACTTTAGAGCAAGACATTTATGTACAAAGTGT 2398
QY 2341 GTCTTGAGGTACAGCGGCTCCTCTGCGGCAATTTGAAAGAAATTCGAGCTTTAGCCCTCTC 2400
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QY 2641 CCAGCCAGCACAGACCTTGTGTGACACCATCCCTCCCGCCAGTGGCAGCTGGGGAGTGG 2700
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US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc.feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A, T, C or G
US-09-392-184-1
Query Match 96.6%; Score 3150.6; DB 3; Length 4858;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3178; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 1 ATGGGAAACCGGAGCGGGCTCCGGGCTCTCGAGCTTTGGGCGCGTACCCAGCTGCTG 60
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QY 61 CTGCTCGCGCGCGCTACTTGGCGCTGTGCGAGCGCACTCGGGCGCGCCCTCCGAGGAGGAC 120
DB 565 CTGCTCGCGCGCGCTACTTGGCGCTGTGCGAGCGCACTCGGGCGCGCCCTCCGAGGAGGAC 624
QY 121 GAGGAGCTAGTGTGTCGGAGCTGGAGCGCGCCCGGGAACAACCGCGCTCCGC 180
DB 625 GAGGAGCTAGTGTGTCGGAGCTGGAGCGCGCCCGGGAACAACCGCGCTCCGC 684
QY 181 CTGACGCGCTTTGACGAGCGAGCTGGATCTGGAGCTGGCGCGCCGACAGCAGCTTTTGGCG 240
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QY 241 CCGCGCTTACGCTCCAGAACGTGGGCGCAATCCGGGTCCGAGAGCGCGCTTCCGGAA 300
DB 745 CCGCGCTTACGCTCCAGAACGTGGGCGCAATCCGGGTCCGAGAGCGCGCTTCCGGAA 804
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DB 805 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 864
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QY 481 CCGGCACTACAGTTTCACTCTCTGCGCGGAATCGGAGGCGCGAGCTAGGCGGCAAG 540
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DB 1225 CGCTATGTGAAACCAATGCTTGTGGCAGACCACTGATGCGAGAAATTCACCGCAGTGT 1284
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DB 1345 CATTGTAATTCAGTTAGCTTGGTGGTGGAGATCTTGGTCTATCCAGATGAACAGAA 1404
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DB 1525 CAGACAGGACTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1584
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QY 1200 TGCAGCGCTTATGGTGTGAAACAGGATTTCCACATGATGGCGCTCAATGCTTTTCCACCT 1259
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QY 1260 GGAACACAGCAGCGCTTGTGTCTCTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1319
DB 1765 GGAACACAGCAGCGCTTGTGTCTCTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1824
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QY 1380 CCGTGGCACTCGTACGATGCGAAACCGGAGTGGCAGTTTACATTTGGGAGGACTCCAA 1439
DB 1885 CCGTGGCACTCGTACGATGCGAAACCGGAGTGGCAGTTTACATTTGGGAGGACTCCAA 1944
QY 1440 AACTGCGCTGTATGAGCAGCAGCAGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1499
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QY 1500 GGT 1559
DB 2005 GGT 2064
QY 1560 GAAATGTGTATCAACCGCAGT 1619
DB 2065 GAAATGTGTATCAACCGCAGT 2124
QY 1620 TTTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGG 1679
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Qy	698	AGAAGCGAATTTGTGTC	CAGTCA	CCGGCTAATGTG	GAAACCAATGCTTGTG	GCGAGACCAAGT	TCGA	757
Db	181	AGAAAGCGAATTTGTGTC	CAGTCA	CCGGCTAATGTG	GAAACCAATGCTTGTG	GCGAGACCAAGT	TCGA	240
Qy	758	TGGCAGAAATTC	CAACGGCAGTGGTCT	TAAGCAATTA	CACTTCTCA	CGTTGTTT	TTCGGTGGCAG	817
Db	241	TGGCAGAAATTC	CAACGGCAGTGGTCT	TAAGCAATTA	CACTTCTCA	CGTTGTTT	TTCGGTGGCAG	300
Qy	818	CCAGATTTGTA	CAACAACCCCAAGCAATTCG	TAAATTCAGTTAG	CCCTGCTG	TGTTGCTG	CAAGATCT	877
Db	301	CCAGATTTGTA	CAACAACCCCAAGCAATTCG	TAAATTCAGTTAG	CCCTGCTG	TGTTGCTG	CAAGATCT	360
Qy	878	TGGTCAATCC	CACGATGAACAG	AGGGGCGGAAAGTGACCT	CCAATGCTG	CGCCCTCACT	CTGCG	937
Db	361	TGGTCAATCC	CACGATGAACAG	AGGGGCGGAAAGTGACCT	CCAATGCTG	CGCCCTCACT	CTGCG	420
Qy	938	GGAACTTTT	TGCAACTG	CGCAGACAGCA	CAACCCAC	CCAGTGAC	CCGGGATG	997
Db	421	GGAACTTTT	TGCAACTG	CGCAGACAGCA	CAACCCAC	CCAGTGAC	CCGGGATG	480
Qy	998	ATGACACAGCA	ATTCCTTTT	CACGACAGACAT	TGTGTGGGT	CCCAGACAT	TGTACTC	1057
Db	481	ATGACACAGCA	ATTCCTTTT	CACGACAGACAT	TGTGTGGGT	CCCAGACAT	TGTACTC	540
Qy	1058	TTGGGATGG	CGTGTGGAACTGTG	TGTATCCG	ACAGCAAGCTGCT	CCGTCA	TAGAAG	1117
Db	541	TTGGGATGG	CGTGTGGAACTGTG	TGTATCCG	ACAGCAAGCTGCT	CCGTCA	TAGAAG	600
Qy	1118	ATGATGCTTT	TACAAGCTGCCTT	CACACAGCCCA	TGAATTAG	GCACGCTGTT	TAAACATGC	1177
Db	601	ATGATGCTTT	TACAAGCTGCCTT	CACACAGCCCA	TGAATTAG	GCACGCTGTT	TAAACATGC	660
Qy	1178	CACATGATGAT	GCAAAAGAGTGTG	CCACAGCCTTAA	TGTTGTGTA	ACCAGGAT	TCCACATGA	1237
Db	661	CACATGATGAT	GCAAAAGAGTGTG	CCACAGCCTTAA	TGTTGTGTA	ACCAGGAT	TCCACATGA	720
Qy	1238	TGGCGTCAAT	GTCTTCCAACTG	GCACACAGCCAGCCTTGG	TCTCCTTGCAGT	GCCTTACA		1297
Db	721	TGGCGTCAAT	GTCTTCCAACTG	GCACACAGCCAGCCTTGG	TCTCCTTGCAGT	GCCTTACA		780
Qy	1298	TGATTCATCAT	TTTTCTGATAATGGT	CATG	GGGGAATGTTTGAT	TGGAACAAGCCT	CAGAATC	1357
Db	781	TGATTCATCAT	TTTTCTGATAATGGT	CATG	GGGGAATGTTTGAT	TGGAACAAGCCT	CAGAATC	840
Qy	1358	CCATACAGCT	CCCCAGGCGATCT	CCCTGG	CACCTCGTACGAT	GCACAA	CCGGCAGTGC	1417
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Db	1081	ACAGAAAGCA	TTTTGATAC	CGCTTTTCA	TGGAAGCT	TGGGGAATGTGGG	GCCTTGGGAG	1140
Qy	1658	ACTGTT	TCAGAACGTG	CCGTGG	AGGATTCAGTAC	CGATCAG	GGGAATGTG	1717
Db	1141	ACTGTT	TCAGAACGTG	CCGTGG	AGGATTCAGTAC	CGATCAG	GGGAATGTG	1200
Qy	1718	TCCCAAGAA	TGGAGGAAGTACT	TGTGA	AGGCAAA	CCAGTGC	GCTACAGATCTCT	1777
Db	1201	TCCCAAGAA	TGGAGGAAGTACT	TGTGA	AGGCAAA	CCAGTGC	GCTACAGATCTCT	1260

Qy	1778	TTGAGGACTGTGCAGACAATAATGGAAAAACCTTTTAGAGAGGGAACAATGTGAAGCACACA	1837
Db	1261	TTGAGGACTGTGCAGACAATAATGGAAAAACCTTTTAGAGAGGGAACAATGTGAAGCACACA	1320
Qy	1838	ACCAGTTTTTCAAAAGCTTCCCTTTTGGGAGTGGGCGCTCGCGTGGAAATGGAATTCGCCAAGTACG	1897
Db	1321	ACGAGTTTTTCAAAAGCTTCCCTTTTGGGAGTGGGCGCTCGCGTGGAAATGGAATTCGCCAAGTACG	1380
Qy	1898	CTGGCGTCTCACCAAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCAATTTGGGTACT	1957
Db	1381	CTGGCGTCTCACCAAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCAATTTGGGTACT	1440
Qy	1958	TCCTTGTTTGGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCCAGATTCACACCTCTG	2017
Db	1441	TCCTTGTTTGGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCCAGATTCACACCTCTG	1500
Qy	2018	TCGTGTGCAAGGACAGTGTGTAAGAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGA	2077
Db	1501	TCGTGTGCAAGGACAGTGTGTAAGAGCTGGTTGTGATCGCATCATAGACTCCAAAAAGA	1560
Qy	2078	AGTTTGTATAAATGTGGTGTGGCGGGGAAATGGATCTACTTGTGTAATAAATAATCAGGAT	2137
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Db	1621	CAGTTACTAGTGCAAAACCTTGGATATCATGATATCATCAAAATTCGCAATTCGAGGCCACCA	1690
Qy	2198	ACATCGAAGTGAAACAGCGGAAACAGAGGGGATCCAGAGAACAAT-GGCAGCTTCTTTGGCC	2256
Db	1681	ACATCGAAGTGAAACAGCGGAAACAGAGGGGATCCAGAGAACAATGGGACGCTTCTTTGGCC	1740
Qy	2257	ATCAAAAGCTGCTGATGGCACATATATCTTAAATGGTGACTACACTTTGTCCACCTTATAG	2316
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Db	1801	CAAGACATTAATGTAACAAAGGTGTGCTTGAGGTGACAGCGGCTCTCTCGCGGCATTTGAA	1860
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Qy	2497	AATGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGCGGAATGTTCTTAAGTCA	2556
Db	1981	AATGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGCGGAATGTTCTTAAGTCA	2040
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Db	2041	TGTCAATTTGGTTGGCAGAGAGACTGGTAGAATGCCGAGACATTAATGACAGCCTGCT	2100
Qy	2617	TCCGAGTGTGCNAAGGAAGTGAAGCCAGCAGCACCACTTGTGAGAGCCATCCCTTCG	2676
Db	2101	TCCGAGTGTGCNAAGGAAGTGAAGCCAGCAGCACCACTTGTGAGAGCCATCCCTTCG	2160
Qy	2677	CCCAGTGGCAGCTGGGGAGTGTGCATCATGTTCTAAGACCTGTGGGAAGGGTTACAA	2736
Db	2161	CCCAGTGGCAGCTGGGGAGTGTGCATCATGTTCTAAGACCTGTGGGAAGGGTTACAA	2220
Qy	2737	AAAAGAAGCTTGAAGTGTCTGCCATGATGAGGGGTGTTATCTCATGAGAGCTGTGAT	2796
Db	2221	AAAAGAAGCTTGAAGTGTCTGCCATGATGAGGGGTGTTATCTCATGAGAGCTGTGAT	2280
Qy	2797	CCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTTCACAAATGCGCAGGAATGCAAGT	2856
Db	2281	CCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTTCACAAATGCGCAGGAATGCAAGT	2340
Qy	2857	GTTTAAGTGGTGTAGCTTTGA-GGCAAGGCCAAAGTAGGAAAGGGCTGGTCAGGGGAAG	2919


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QY 2012 CCTCTGTCGTGTCAGGACAGTGTGTAAGAGCTGGTGTGATCGCATCATGACTCCA 2071
Db 1343 CCTCTGTCGTGTCAGGACAGTGTGTAAGAGCTGGTGTGATCGCATCATGACTCCA 1402
QY 2072 AAAAGAAATTTGATAATGTTGGTGTTCGGGGGAAATGATCTACTTGTAAAAAATAT 2131
Db 1403 AAAAGAAATTTGATAATGTTGGTGTTCGGGGGAAATGATCTACTTGTAAAAAATAT 1462
QY 2132 CAGGATCAGTTACTAGTGCAGAAACCTGGATATCATGATATCATCACAATTCCAACTGGAG 2191
Db 1463 CAGGATCAGTTACTAGTGCAGAAACCTGGATATCATGATATCATCACAATTCCAACTGGAG 1522
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Db 1523 CCACCAATCGAAGTGAACAGCGGAACAGAGGGGATCCAGGAACAATGGCAGCTTTC 1582
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QY 2432 TGGGCAATGCCCTTCGACCTTAATAATTAACACCTACTTCGTAAGAAGAGGAAT 2491
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QY 2492 CTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCAATGTTCTA 2551
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QY 2552 AGTCATGTGAATTTGGGTTGGCAGAGAAGTGTGTAGAAATGCCAGACATTAATGGACAGC 2611
Db 1883 AGTCATGTGAATTTGGGTTGGCAGAGAAGTGTGTAGAAATGCCAGACATTAATGGACAGC 1942
QY 2612 CTGCTCCGAGTGTGAAAGAAAGTGAAGCCAGCAGCAGACCTTGTGCGACCATC 2671
Db 1943 CTGCTCCGAGTGTGAAAGAAAGTGAAGCCAGCAGCAGACCTTGTGCGACCATC 2002
QY 2672 CCTGCCCCAGTGCAGCTGGGGAGTGGTCAATCATGTTCTTAAGACCTGTGGGAAGGTT 2731
Db 2003 CCTGCCCCAGTGCAGCTGGGGAGTGGTCAATCATGTTCTTAAGACCTGTGGGAAGGTT 2062
QY 2732 AAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCT 2791
Db 2063 AAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCT 2122
QY 2792 GTGATCCTTTAAAGAAACCTTAACATTTATAGACTTTTGGCAATGGCGAATGCAAGTT 2851
Db 2123 GTGATCCTTTAAAGAAACCTTAACATTTATAGACTTTTGGCAATGGCGAATGCAAGTT 2182
QY 2852 AA 2853
Db 2183 AA 2184
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RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-13

Query Match 50.8%; Score 1655; DB 4; Length 2184;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

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QY 671 AGCCCAAGAACTCGAAGCATTAAGAAGAGCGATTTGTGTCAGTCCAGTCTATGTGG 730
Db 2 AGCCATCAGGACCAGGAAGCATTAAGAAGAGCGATTTGTGTCAGTCCAGTCTATGTGG 61
QY 731 AAACCATGCTGTGGCAGACCACTGCATGTCAGAAATTCACGCGCAGTGGTCTAAAGCAT 790
Db 62 AAACCATGCTGTGAGTGCACCACTGCATGTCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 121
QY 791 ACCTTCTCAGTGTGTTTGGTGGCAGCCAGATGTGTACAAACACCCAGCATTCGTAAAT 850
Db 122 ACCTTCTCAGTGTGTTTGGTGGCAGCCAGATGTGTACAAACATCCAGCATTCAGTAAT 181
QY 851 CAGTTAGCTGTGGTGGTGAAGATCTTGGTGCATCCAGCATGACAGAGGGCCGAG 910
Db 182 CAATTAGCTGTGGTGGTGAAGATCTTGGTGCATATACAGGAGCAGAGGACCAAG 241
QY 911 TGACCTCCAAATGCTGCGCTCACTCTCGGAACTTTTGCAACTGGCAGAGCAGCAAC 970
Db 242 TTACCTCCAAATGAGTCTCACCTTCGGAATTTCTGCAGTGGCAGAAACACACA 301
QY 971 CACCCAGTGAACCGGATGACAGACATATGACAGCAATTCCTTTCCAGCAGAGACT 1030
Db 302 GCCCAGTGAACCGGATCCAGAGCACTATGACATGCAATTCCTTTCCAGCAGAGACT 361
QY 1031 TGTGTGGTCCAGACATGATGATCTTGGGATGGCTGATGTGGAACTGTGTGATC 1090
Db 362 TATGTGGTCCCAACAGTGTGACACTCTCGGAATGGCAGATGTTGGAACCGTATGTGACC 421
QY 1091 CGAGCAGAAAGCTGCTCGTCTATAGAAGATGATGTTTACAAGCTGCCTTCACCAAGCCC 1150
Db 422 CAGCAGGAGCTGCTCAGTCTATAGAAGATGATGTTTGAAGCTGCTTCACCAAGCCC 481
QY 1151 ATGAATTTAGGCCACGTGTTTAAACATATGCAATGCAATGATGATGCAAGAGTGTGCCAGCTTA 1210
Db 482 ATGAATTTAGGCCACGTGTTTAAACATATGCAATGCAATGATGATGCAAGAGTGTGCCAGCTTA 541
QY 1211 ATGCTGTGAACAGGATTCACCATGATGTCCTTCCAACTGGACCCAGCAGCC 1270
Db 542 ATGCTGTGAGTGGGAGTTCATCATGATGGCTCGATGCTCTCCAGCTTACCATAGCC 601
QY 1271 AGCTTGGTCTCTTGGAGTGCCTTACATGATTAACATTTCTGGATAAATGTTGATGGG 1330
Db 602 AGCTTGGTCACTTGGAGTGCCTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 1331 AATGTTTGTGAGCAAGCCCTCAGAAATCCCATACAGTCCAGGCGATCTCCCTGGCACCT 1390
Db 662 AATGTTTGTGAGCAAGCCCTCAGAAATCCCATACAGTCCCTTCTGATCTTCCCGGTACCT 721
QY 1391 CGTACGATGCCAACCGGAGTGCAGTTCATTTGAGGAGGAGTCCAAACACTGCCCCCTG 1450
Db 722 TGTACGATGCCAACCGGAGTGCAGTTCATTTGAGGAGGAGTCCAAACACTGCCCCCTG 781
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1451 ATGAGCCAGCACATGTAGCACCTTGTGTGTGTACCGGCACCTCTGGTGGGTGCTGGTGT 1510
Db |||||
782 ATGAGCCAGCACATGTACTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
Qy |||||
1511 GTCAAAACCAAAACATTTCCCGTGGGGGATGGGCACAGCTGTGTGAGAGAGGAAATGGTGT 1570
Db |||||
842 GCCAAACCAAAACATTTCCCTTGGGCAGATGGGCACAGCTGTGTGAGAGAGGAAATGGTGT 901
Qy |||||
1571 TCAAGCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATCGCTTTTCATGGAA 1630
Db |||||
902 TCAGTGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATCGCTTTTCATGGAA 961
Qy |||||
1631 GCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTTCGGTGGAGAGTCCAGT 1690
Db |||||
962 GCTGGGGAATGTGGGGACCGTGGGAGACTGTTCGAGAACCTGTGTGGTGGAGTTCAT 1021
Qy |||||
1691 ACAGATGAGGGAATGTGACAAACCGAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGCA 1750
Db |||||
1022 ACACATGAGGAATGTGACAAACCGAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGCA 1081
Qy |||||
1751 AACGATGGCTACAGATCTCTTAACCTTTGAGGACTGTCCAGACAAATATGGAAGAACT 1810
Db |||||
1082 AACGATGGCTACAGATCTCTTAACCTTTGAGGACTGTCCAGACAAATATGGAAGAACT 1141
Qy |||||
1811 TTAGAGGAACAAATGTGAAGCACACACGAGTTCCTTGAAGCTTCCTTGGGAGTGGG 1870
Db |||||
1142 TCAGAGAGAGCAGTGGGAGGCGCAATGAGTTCCTTGAAGCTTCCTTGGGAGTGGG 1201
Qy |||||
1871 CTGGGTGGAATGGATTCCTCAAGTAGTCCGCTGCTCACAAAGGACAGGTGCAAGCTCA 1930
Db |||||
1202 CCAGTGTAGGTGGACACCCAGTAGTCCGCGGCTCTCGCAAGGACAGGTGCAAGCTCA 1261
Qy |||||
1931 TGTGCAAGCCAAAGCATTTGCTACTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1990
Db |||||
1262 CCGTGTGAAGCCAAAGCATTTGCTACTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1321
Qy |||||
1991 CTCATGTAGCCAGATTCACCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2050
Db |||||
1322 CTCCTGTAGTCCAGACTTACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1381
Qy |||||
2051 GTGATCGCATATAGATCTCAAAAGAGAGTGTGATAAATGTGTGTGTGTGTGTGTGTGTGT 2110
Db |||||
1382 GTGATCGCATATAGATCTCAAAAGAGAGTGTGATAAATGTGTGTGTGTGTGTGTGTGTGT 1441
Qy |||||
2111 GATCTACTGTGATAAATATCAGATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2170
Db |||||
1442 GTTCCACATGCAAGAGATGTGAGGAATAGTCACTAGTACAGACCTTGGGTATCATGACA 1501
Qy |||||
2171 TCATCACAATTCCACTGGAGCCACCAATCGAAGTGAACAGCGGACACAGAGGGAT 2230
Db |||||
1502 TTGTCAATTCCTGTGTGAGCCACCAATCGAAGTGAACAGCGGACACAGAGGGAT 1561
Qy |||||
2231 CCAGGAACAAATGGCAGCTTTTGTCCATCAAAAGCTGTGTGATGCAATATATTTTAATG 2290
Db |||||
1562 CCAGGAACAAATGGCAGCTTTTGTCCATCAAAAGCTGTGTGATGCAATATATTTTGAATG 1621
Qy |||||
2291 GTGACTACACTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGGTGTGTGTGTGTGT 2350
Db |||||
1622 GAAATTCATCTGTGTCCACATAGAGCAAGACCTCACCTTACAAAGGTGTGTGTGTGTGT 1681
Qy |||||
2351 ACAGCGCTCTCTGTGGGCAATTTGGAAGAAATTCGAGCTTTTGAAGCTTCTCAAGAGCCCT 2410
Db |||||
1682 ACAGTGGTTCCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1741
Qy |||||
2411 TCACCATCAGGTTCTTACTGTGGGCAATGCGCTTTCGACCTAAATTTAAATACACTACT 2470
Db |||||
1742 TAACCATCAGGTTCTTATGTGTAGGCAATGCTCTCGACCCCAAAATTTAAATTTCACTACT 1801
Qy |||||
2471 TCGTAAAGAGAGAGGATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATG 2530
Db |||||
1802 TTATGAAGAGAGAGAGAGAGATCATTCACGCAATTCCTCCACATTTTCTGTAGTGGGTATG 1861

2531 AAGATGGGGCGAATGTTCTAAGTCTATGTGAATTTGGTTGGCAGAGAGACTGGTAGAAT 2590
Db |||||
1862 AAGATGGGGCGAATGTTCTAAGTCTATGTGAATTTGGTTGGCAGAGAGACTGGTAGAAT 1921
Qy |||||
2591 GCCGAGACATTAATGGACAGACCTCTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGCA 2650
Db |||||
1922 GCAGAGACATTAAGCGACACCTCTCTCGAATGTGCAAGGAAAGTGAAGCCAGCCAGTA 1981
Qy |||||
2651 CCAGACCTTGTGCAGACACCTCTCTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGTA 2710
Db |||||
1982 CCAGACCTTGTGCAGACACCTCTCTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGTA 2041
Qy |||||
2711 CTAACACCTTGTGGGAGGTTTACAAAAGAAAGCTTGAAGTGTCTGCCATGATGGAG 2770
Db |||||
2042 CCAAACTTGTGGGAGGTTTACAAAAGAAAGCTTGAAGTGTCTGCCATGATGGAG 2101
Qy |||||
2771 GGGTGTATCTCATGAGAGCTGTGATCTTTTAAAGAAACCTAAACATTTTCATAGACTTTT 2830
Db |||||
2102 GCGTGTATCAATGAGAGCTGTGATCTTTTGAAGAAAGCAAGCATTACATTGACTTTT 2161
Qy |||||
2831 GCACATGCGCAATGCGAGTTAA 2853
Db |||||
2162 GCACATGCGCAATGCGAGTTAA 2184

RESULT 7

US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610

GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8

LENGTH: 3638
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (278)..(2992)
; NAME/KEY: misc.feature
; LOCATION: (3636)
; OTHER INFORMATION: n = T

US-09-369-364A-8

Query Match 20.4%; Score 666.2; DB 3; Length 3638;
Best Local Similarity 56.1%; Pred. No. 1.6e-145;
Matches 1544; Conservative 0; Mismatches 1123; Indels 84; Gaps 12;

Qy 56 TGCTGCTGTCTGCCGCGCGCTACTTGGCGTGTGCGAGCAGCACTCGGGCGCCCTCCGAGG 115
Db |||||
330 TCGAGCTGCGCGCGCGCACTCTGCTGCGAGAGCCCGGGCGCGGAAACGGGGCGC 389
Qy 116 AGGACGAGAGGTAGTGTGCGGAGCTGGAGCGCGCCCGCGGACACGCGGC 175
Db |||||
390 AGGCTCGAGCTAGTGTGCGCGCTTCCCGCAGCGAGCGAGCTGCG---CT 446
Qy 176 TCGGCTCGAGCTTTCAGCAGAGCTGGATCTCGAGCTGCGGCGCGGACAGAGCTTTT 235
Db |||||
447 TCACCTGTGCGCTTCGGCCAGGGCTTCTGCTGGCTTGGCGCTGAGCCAGCTTCC 506
Qy 236 TGGCGCCCGGCTTTCAGCTTCCAGAACTGGGGCGCAAAATCCGGGTCCGAGAGCGCGCTTC 295
Db |||||
507 TGGCGCGGAAATTCAGATCGAGCGCTTCGGGG-----CTCGAGCGCGCGCGGG 560
Qy 296 CGGAAACCGACTTGGCGCAGCTGCTTCTACTCGGACCGGTGAATGGCGATCCAGCTCGG 355
Db |||||

QY 2492 -----CTTTCAATGCTATCCCACTTTT 2515
Db 2766 TCAGCGTCAGAAATAGCAAGGAAGCAACCAACATCATTCAGTCACCTGCCTCTG 2825
QY 2516 CAGCATGGGTCAATGAAGAGTGGGCGAATGTTCTTAAGTCATGTGAATGGGTGGCAGA 2575
Db 2826 CGAGTGGGTCTTGGGAGACTGGTCTGAATGTCGAGACAGTGCAGAGGTAGCTGGCAGC 2885
QY 2576 GAAGACTGTAGATGCCAGACATTAATGGACAGCTCTCCGAGTGTGCAAGGAAG 2635
Db 2886 GCGGACTGTGAATGCAAGGACCCCTCAGGTCAAGCTCTGACACTGTGATGAGGCTC 2945
QY 2636 TGAAGCAGCCAGCAGACACTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGG 2695
Db 2946 TGAACCTGAGATGCCAAGCCCTGTGGAGCAGCGGTGTCCCTCTGATCCCTTGGT 3005
QY 2696 AGTGTGTCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAGAGCT 2746
Db 3006 GGAATCTCTTAGGCTTATGGATTTGGGCTACTGGTGTAAACAGACAAAGGT 3056

RESULT 8
US-10-009-332-2
; Sequence 2, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGRECANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-332-2

Query Match 19.3%; Score 629.8; DB 4; Length 2853;
Best Local Similarity 57.1%; Pred. No. 4,8e-137;
Matches 1306; Conservative 0; Mismatches 912; Indels 69; Gaps 6;

QY 187 GCCTTTGACAGCAGCTGGATCTGGAGCTGCGGCCCGCAGCAGCAGCTTTTGGGCGCCCGC 246
Db 175 GCATTTGAGGAGACTTTTACCTACACTGACCGCGGATGCTCAGTTCTTGGCTCCCGC 234
QY 247 TTCAGCTCCAGAACGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGAACCGAC 306
Db 235 TTCTCCACTGAGCATCTGGGCGTCCCTTCCAGGGGCTCACCGGGGGCTC---TTCAGAC 291
QY 307 CTGGCGCACTCTTACTCCGCGCAGCGGATGGGATCCAGCTCGGCTCGGCTCGGCTC 366
Db 292 CTGGCAGCTGCTTCTATTCTGGGACGTGAACCGCGAGCCGAGCTCTGCTGCTG 351
QY 367 AGCCTCTGGAGGGCGTGGCGGCGCTTCTACTGCTGGGGGAGCGGTATTTCTATCCAG 426
Db 352 AGCCTCTGGGGGGCTCCCGGAGGCTTTGGCTACCGAGGCGCGGATGTGCTATTAGC 411
QY 427 CCGCTGCCCGCCAGCAGCGCTTCGCCACCGCGCCCGCAGGGGAGAACCGCGGCA 486
Db 412 CCGCTGCCCAATGTAGCGCGC- CGGCGGCGAGCGCAACAGCAGGGCGCACACCTTCT 470
QY 487 CCACCTACAGTCCACCTCTCGCGGCGGAATCCGAGGGGAGCTAGCGGCGACGTGCGG 546
Db 471 CCAGCGCCGGGTGTTCCGGGCGGGCTTCCGAGACCCCACTCTCTCGCTCGGGGTG 530
QY 547 GTCTGGACGACGAGCGCCCGCGCACTGGGAAAGCGGAGACCGAAGACGGAAGGG 606

Db 531 CTCGGGCTGGAACCCCGCCATCTCAGGCGCTTGACCCCTTACAGCCGCGGCGGCGG 590
QY 607 ACTGAGGGGAGGAGCAAGAGGCTCAGTGGTCCGCGCAGGACCCCGGCACTGCAAGCGGTA 666
Db 591 CTTTCGGGAGAGTCTAGCCGCGCAGGTCTGGGCGC----- 627
QY 667 GGACAGCCCAAGGAACTGGAAGCATAGAAAGAACGATTTGTGTCAGTCAACGCTAT 726
Db 628 -----GCCAGCGTTTCGTGTCTATCCCGCGGTAC 657
QY 727 GTGGAAACCATCTTGTGGCAGACCATGATGGCAGAAATCCACGGCAGTGGTCTTAAG 786
Db 658 GTGGAGACGCTGGTGTGCGGACGAGTCAATGGTCAAGTTCACGGCGCGACCTGGAA 717
QY 787 CATTACCTTCTCAGCTTGTGTTTCGGTGGCAGCAGATGTACAACACCCAGCATTCGT 846
Db 718 CATTATCTGCTGACGCTGTGCAACGCGCGCGGACTCTACCGCATCCAGCATCTCTC 777
QY 847 AATTCAAGTTAGCTGTGTGTGAAGATCTTGTGTCATCCAGATGAACAGAAAGGGCG 906
Db 778 AACCCCATCAATCGTTGTGTCAAGGTGCTGCTTCTTAGAGATGCTGACTCCGGGCCC 837
QY 907 GAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGAACCTGGCAGAGCAGAC 966
Db 838 AAGGTCAACGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCTGGCAGAAAGCTG 897
QY 967 AACCCACCCAGTGCAGGATGCAGACGACTATGACAGCAATTTCTTTACCAGACAG 1026
Db 898 AACAAAGTGAGTGACAAAGCACCCCGAGTACTGGGACACTGCCATCTCTTTCCAGGCG 957
QY 1027 GACTTGTGTGGTCCCGACAGATGTCATCTCTTGGATGGCTGATGTTGGAATGTGTGT 1086
Db 958 GACCTGTGTGGAGCACCACTGTGACACCTTGGGCAATGGCTGATGTGGGTACCATGTGT 1017
QY 1087 GATCCGAGCAGAGCTGCTCCGTCTATAGAAGATGATGTTTCAAGCTGCCCTTACCACA 1146
Db 1018 GACCCCAAGAGAAGCTGCTCTGCTATGAGGAGATGGGCTTCCATCAGCCTTCACT 1077
QY 1147 GCCATGAATAGGCGACGTGTTTAACTGCCACATGATGATGCAAGCAGTGTGCCAGC 1206
Db 1078 GCCCAGAGCTGGGCGCAGTGTTCACATGCCCCCATGAACATGTGAAAGTCTGTGAGGAG 1137
QY 1207 CTTAATGTTGTAACCCAGGATTTCCACATGATGGGTCAATGCTTTCACACTGGACAC 1266
Db 1138 GTGTTTGGAGAGCTCGAGCGCAACACATGATGTCCCGACCTCATCCAGATCGACCT 1197
QY 1267 AGCCAGCTTGTCTCTTTCAGTGCCTACATGATTAATCATTTCTGTGATTAATGTCTAT 1326
Db 1198 GCCAACCCCTGTGCTGAGCTGCTGCTCATCATCCAGCTTCTGTGACAGCGGCGAC 1257
QY 1327 GGGGAATGTTGATGGACAGGCTCAGATCCCATACAGTCCCGAGCGATCTCCCTGGC 1386
Db 1258 GGTGATGCTCTCGACCAACCCAGCAAGCCCATCTCCCTGCGGAGGATCTGCGCGGC 1317
QY 1387 ACCTCGTACGATGCAACCCGAGTGCCTGTTTATATTTGGGGAGGACTTCCAAACACTGC 1446
Db 1318 GCGAGTACACCTGAGCCAGCAGTGGGCTGGCTTGTGGCTGGGCTTCCAGCCCTGT 1377
QY 1447 CTTGATGACGACGACATGATAGCACTTGTGGTGTACCGGCACTCTCTGGTGGGGTGTG 1506
Db 1378 CTTTACATGCACTAC---TGACCAAGCTGTGTGTGTCACCGGAAGGCCAAGGACAGATG 1434
QY 1507 GTGTGTAACCAACCAACACTTCCCGTGGGCGGATGCCACAGCTGTGGAGAAAGGAATGG 1566
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QY 1567 TGTATCAACCGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGTATAGCGCTTTTCA 1626
Db 1495 TGCTCTCAAGGGGCTGCTGTGGAGACACAACCTCAA-----CAAGCACAGGGTGGAT 1548
QY 1627 GGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTTCAGAAACGTGCGGTGGAGAGTC 1686

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Db 1549 GGTTCCTGGGCCAAATGGGATCCTATGGCCCTGCGGCACATGTGTGGGGCGTG 1608
Qy 1687 CAGTACACGATGAGGGAATGTGACACCCAGTCCCAAGATGAGGGAGTACTGTGA 1746
Db 1609 CAGCTGGCCAGGAGGAGTGCACCAACCCACCCCTGCCAACCGGGGCAAGTACTGGAG 1668
Qy 1747 GGCACAAACGAGTGGCTACAGATCCTGTAACTCTTGAGGACTGTCCAGAC---AATAATGGA 1803
Db 1669 GGAGTGAAGGTGAATAACCATCTGCAACTCTGGAGCCCTGCCAGCTCAGCTCCGGA 1728
Qy 1804 AAAACCTTTAGAGAGGAACAATGTGAAGACACAAACGAGTTTCAAAGCTTCCTTTGGG 1863
Db 1729 AAGAGCTTCCGGGAGGAGAGTGTGAGGCTTTCAACCGCTTACAAACACACAGCACCAACCGG 1788
Qy 1864 AGTGGGCTCGGTGGGAATGGAATCCCAAGTAGCTGGGCTCTCACCAAGAGCAGGTGC 1923
Db 1789 CTCACCTCTCGCCGTGGCATGGGTGCCCAAGTACTCCGGCGTGTCTCCCGGGHCAAGTGC 1848
Qy 1924 AAGCTCATCTGCCAAGCAAGGCAATGGCTACTCTTCTTCTTGGCAGCCCAAGGTTGTA 1983
Db 1849 AAGCTCATCTGCCGAGCAATGGCATGGCTACTCTTCTATGTGCTGGCACCACCAAGGTGGT 1908
Qy 1984 GATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAATA 2043
Db 1909 GACGCGACGCTGTGCTCTCTGACTCCACCTCGTCTGTGTGCAAGGCAAGTGCATCAAG 1968
Qy 2044 GCTGGTGTGATCGCATATAGACTCCAAAGAGTTTGTATAAATGTGGTGTTCGGG 2103
Db 1969 GCTGGCTGTGATGGGAACCTGGGCTCCAAAGAGATTCGACAAAGTGTGGGTGTGGG 2028
Qy 2104 GGAATGGATCTACTTGTAAAAAATATCAGGATCAGTACTAGTGCAAAACCTGGATAT 2163
Db 2029 GGAGACATTAAGCTGCAAGAGGTGACTGGACTCTTACCAAGCCATGCAATGGCTAC 2088
Qy 2164 CATGATATCATCAATTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAACAG 2223
Db 2089 AATTCGTGGTGGCCATCCCGCAGGCGCTCAAGCATCGACATCCCGCAGCGCGTTAC 2148
Qy 2224 AGGGATCCAGGACATGCGAGTCTTCTGGCCATCAAGCTGCTGATGGCCACATATT 2283
Db 2149 AAAGGGCTGATCGGGGATGCAACTACTCTGCTCTGAAGAACAGCCAAAGGCAAGTACTG 2208
Qy 2284 CTTAATGGTCACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTGTC 2343
Db 2209 CTCAACGGGATTTCTGTGGTGTGGCGGTGGAGCGGACCTGTGGTGAAGGGCAGTCTG 2268
Qy 2344 TTGAGGTACAGCGGCTCTCTGCGGCATGTGAAGAAATTCGACGTTTACGCCCTCTCAAA 2403
Db 2269 CTGGGTACAGCGGCACGGGCACAGCGGTGGAGAGCCTGCAAGGCTTCCCGGCCCATCTG 2328
Qy 2404 GAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATATC 2463
Db 2329 GAGCCGCTGACCGTGGAGGCTCTCTCCGTGGGGAAGATGACACCGCCCGGGTCCGCTAC 2388
Qy 2464 ACCTACT 2470
Db 2389 TCCTTCT 2395
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RESULT 9

US-09-122-126B-1

; Sequence 1, Application US/09122126B

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122.126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 4192

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-122-126B-1
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Query Match 18.5%; Score 603.4; DB 3; Length 4192;

Best Local Similarity 59.7%; Pred. No. 8.3e-131;

Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

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Qy 686 GAAGCATAGAAGAAAGACGATTTGTGTCCAGTCCAGCTATGTGGAACCATGTTGTGG 745
Db 1022 GAGCCGAAAGAGCAAGCGCTTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGG 1081
Qy 746 CAGACAGATCGATGGCAGAAATCCACGGCAGTGTCTTAAAGCATTACTTCTCACGTTGT 805
Db 1082 CAGATGACAAGATGGCGGCATTCACGGTGGGGGCTTAAAGCGCTACTCTCTACAGTGA 1141
Qy 806 TTTTCGGTGGCAGCCAGATTTGTACAAACACCCACAGCATTCGTAAATTCAGTTAGCTGGTGG 865
Db 1142 TGGCAGCAGCAGCCAAGGCCCTTCAAGCACCCCAAGCATCCGCAATCCTGTGAGCTTGGTGG 1201
Qy 866 TGGTGAAGATCTTTGGTCATCCACGATGAACAGAAAGGGGCCGGAAGTACACCTCCATGCTG 925
Db 1202 TGACTCGGCTAGTGTATCTGGGGTCAGGCGAGGAGGGGGCCCAAGTGGGGCCCAAGTGTCTG 1261
Qy 926 CCCTCACTCTGCGGAACCTTTTGCAACTGGCAGAAGCAGCACAAACCCACAGTGACCCGGG 985
Db 1262 CCAGACCCCTGGCGAGCTTCTGTGCTGGCAGGCGGGGCTTCAACACCCCTGAGGACTCGG 1321
Qy 986 ATGCAGAGCACTATGACACAGCAATTTCTTTTACACAGACAGGACTTGTGTGGGTCCAGGA 1045
Db 1322 ACCCTGACCACTTTTGACACAGCCATTTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCA 1381
Qy 1046 CATGTGATCTCTTTGGGATGGCTGATGTTGGAACCTGTGTGTGATCCGAGCAGAGCTGCT 1105
Db 1382 CTTTGGCACACGCTGGGTATGGCTGATGTGGGCAACCGTCTGTGACCCGGCTCGGAGCTGTG 1441
Qy 1106 CCCTCATAGAAGATGATGGTTTACAAAGCTGCCCTTACCACAGCCCATGAATAGGCCACG 1165
Db 1442 CCATTTGGAGGATGATGGGCTCCAGTCAAGCTTCTGCTGCTCATGAATGGGTCTATG 1501
Qy 1166 TGTTTAATCATGCCACATGATGATGCAAAAGCAGTGTGCCAGCTTTAATGG---TGTGAACC 1222
Db 1502 TCTTCAACATGCTCCATGACAACTCCAAAGCATGATCATGATTTGAAATGGGCTTTGAGCA 1561
Qy 1223 AGGATTTCCACATGATGGCGCTCAATGCTTTCCAACTGGACCAACAGCCAGGCTTGGTCTC 1282
Db 1562 CCTCTCGCCATGTATGGCCCTGTGATGGCTCATGTGSGATCCTGAGGAGGCCCTGGTCCC 1621
Qy 1283 CTTTGCAGTGCCTACATGATTTACATCATTTTCTGGATATGTCATGCGGGAATGTTTGAATGG 1342
Db 1622 CTTGCAGTGCGGCTTTCATCACTGACTTCTCTGGACAATGGCTATGGGCACTGTCTCTTAG 1681
Qy 1343 ACAAGCTCAGAAATCCCATACAGCTCCCGAGCGCATCTCCCTGGCACCCTCGTACGATGCCA 1402
Db 1682 ACAAACAGAGGCTCCATTGCAATCTGCTGTGACTTTTCCCTGGCAAGGACTATGATGCTG 1741
Qy 1403 ACCGGCAGTGCACGATTTTACATTTTGGGGAGGAGCTCCAAACACTGCGCTGTATGACCCAGCA 1462
Db 1742 ACCGCCAGTGCAGCTGACCTTCCGGGCCGCACTCACGCCATTTGTCCACAGCTGCGCGCGC 1801
Qy 1463 CATGTAGCACCTTCTGGGTGTACCGGCACCTCTGGTGGGGTGTCTGGTGTGTCAAACCAAAAC 1522
Db 1802 CCTGTGTCGCCCTCTGGTGTCTTGGCCACCTCAATGGCCCATGCCATGTGCCAGACCAAAAC 1861
Qy 1523 ACTTCCCGTGGGCGGATGGCACACAGCTGTGTGAGAGAGGGAATGTGTATCAACCGCAAGT 1582
Db 1862 ACTCGCCCTGGGCGGATGGCACACCTCTCGGGCCCGCACAGGCTGTCATGGGTGGTCTGCT 1921
Qy 1583 GTGTGAACAAACACGACAGAAAGCATTTTGTGATAGCCCTTTTTCATGGAAGCTGGGGAATGT 1642
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Db 1922 GCCTCCACATGACACAGCTCCAGGACTTCAATATATCCACAGGCTGGTGGGTCTCTT 1981
Qy 1643 GGGGGCTTGGGGAGACTGTTTCAGAAACGTGGGTGGAGGAGTCCAGTACAGATGAGGG 1702
Db 1982 GGGGACCAATGGGTGACTGCTCTCGGACCTGTGGGGTGGTGTCCAGTTCTCTCCCGAG 2041
Qy 1703 AATGTGACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGCAAAACAGTGGCGT 1762
Db 2042 ACTGCAGAGGCTGTCCCGGAATGGTGGCAAGTACTGTGAGGGCCGCCGTACCCGCT 2101
Qy 1763 ACAGATCTCTGTAACTTGAAGACTGTGCCAGACAAATAATGGAATAAACTTTAGAGGAAAC 1822
Db 2102 TCCGCTCTCTCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGC 2161
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Qy 1883 GGATTTCCCAAGTACGCTGGCGTCTCAACAAAGGACAGGTGCAAGCTCATCTGCCAAGCCA 1942
Db 2222 GGGTTCCTCGCTACACAGGCTGGGCCCCCAAGACCAAGTGCAAACTCACTGCCAGGCC 2281
Qy 1943 AAGCAITGGCTACTTCTTCGTTTTGACGCCCAAGTTGTAGATGATCTCCATGTAGCC 2002
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Qy 2003 CAGATTCACCTCTGCTGTGCGAGGACAGTGTAAAGCTGGTGTGATCGCATCA 2062
Db 2342 CGGACAGCTCTCTGGTGTGTCAGAGGCCGATGATCCATGCTGGCTGTGATCGCATCA 2401
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Db 2402 TTGGCTCCAAAGAGAGTTTGAACAGTGCATGTGTGCGAGGGACGGTCTGGTTGCA 2461
Qy 2123 AAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAATTC 2182
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Qy 2360 CTTCTGGCGCATTTGGAAGAAATTCGCAGCTTTAGCCCTTCAAGAGCCCTTGACCATCC 2419
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Qy 2420 AGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATATACACTTCTTCTGT 2474
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RESULT 10

US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-634-286A-1

Query Match 18.5%; Score 603.4; DB 4; Length 4192;
Best Local Similarity 59.7%; Pred. No. 8,3e-131;
Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

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Db 1202 TGACTCGGCTAGTGTATCTTGGGGTCAAGCGAGAGGGGCCCAAGTGGGGGCCCAAGTGTG 1261
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Db 1262 CCCAGACCTTGGCAGCTTCTGTGCTTGGCAGCGGGGCTCAACACCCCTGAGGACTCGG 1321
Qy 986 ATGCAGAGCACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTTGTGTGGTCCCAGA 1045
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Qy 1046 CATGTGATCTCTTGGGATGGCTGATGTGTGAACCTGTGTGTGATCCGAGCAGAGCTGCT 1105
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Db 1742 ACCGCGAGTCCAGCTGACCTTTCGGGCCCGGACTCAAGCCATTTGTCCAGAGCTGCGCCGC 1801
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Qy 1583 GTGTGAACAAACCCGACAGAAAGCATTTTGATACGCTTTTTCATGTGAAGCTGGGAATGT 1642

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Qy 1643 GGGGGCTTGGGAGAGCTGTTCCAGAACGTCGGTGGAGAGTCCAGTACACGATCAGGG 1702
Db 1982 GGGGACATGGGGTGAAGTCTTCGAGACCTGTGGGGTGTGTCCAGTCTTCTCCCGAG 2041
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Db 2222 GGGTCTCTCTACACAGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCAGGCC 2281
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Db 2282 GGGCACTGGGCTACTATATGTGCTGGAGCCACGGGTGGTAGATGGAGCCCTGTTCCT 2341
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Db 2342 CGGACAGCTCTCGGCTGTGTCCAGGCCGATGCATCCATGCTGCTGTGATCGCATCA 2401
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Qy 2360 CCTCTGGGCAATGGAAAGATTCGACGCTTACGCTTACGCTTCAAGAGCCCTTCACCATCC 2419
Db 2696 CCACTGAGCCTCAGAGACACTGTGAGGCCATGGGCCACTTGGCCAGCCCTTTCAGACTGC 2755
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Db 2756 AGTCTAGTGGCTGGCAACCCCGAGCACACAGCCCTCCGATACAGCTTCTTGT 2810

RESULT 11
US-10-247-685-1
; Sequence 1, Application US/10247685
; Patent No. 6753176
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (406)...(2916)
US-10-247-685-1

Query Match
Best Local Similarity 18.5%; Score 603.4; DB 4; Length 4192;
Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

Qy 686 GAAGCATAGAAGAAGACGATTTGTCTCAGTCAACGCTATGTGGAACCATCTGTGTGG 745
Db 1022 GACCCGAAAGAGCAAGCGCTTGTCTTCTAGTAGATTTGTGGAGACATCGGTGGTGG 1081
Qy 746 CAGACAGTTCGATGGCAGAAATTCACGGCAGTGTCTAAAGCATTAACCTTCTCACGTTGT 805
Db 1082 CAGTGAAGATGGCGCATTCACGGTGGGGGCTAAAGCGCTACTCTCTAACAGTGA 1141
Qy 806 TTTCCGTTGGCAGCAGATTTGTACAAACACCCAGCAATTCGTAAATCAGTTAGCTGGTGG 865
Db 1142 TGGCAGCAGCAGCAAGGCTTCAAGCACCACCAAGCATCCGCAATCTGTCTCAGCTGGTGG 1201
Qy 866 TGGTGAAGATCTTGTCTCATCCAGATGAACAGAGAGGGGCGGAGTGAACCTCCAAATGCTG 925
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Qy 1283 CTTGCACTGCTTACATGATTTACATCATTTCTGGATATGTCATGCGGAATGTTTGTATGG 1342
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Db 1982 GGGGACCATGGGGTGAATGCTCTCGAGACCTGTGGGGTGGTTCAGATTTCTCTCCCGAG 2041
QY 1703 AATGTGACAAACCAAGTCCCAAGAAATGGAGGAAGTACTGTCAAGCAAAACAGTGGCT 1762
Db 2042 ACTGACAGAGGCTGTCTCCCGGAATGGTGGCAAGTACTGTGAGGCGCCCTTACCCGCT 2101
QY 1763 ACAGATCTCTGTAACTTGAAGCTGTCCAGACAATAATGAAAAACCTTTAGAGAGAAC 1822
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Db 2222 GGGTTCCTCGCTACACAGCGTGGCCCCCAGGACCAAGTGGTGTAGTGGACCCCTGTGCC 2281
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Db 2282 GGGCACTGGCTACTACTATGTGCTGGAGCCAGCGTGTGTAGTGGACCCCTGTGCC 2341
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QY 2063 TAGACTTCCAAAAGAAATTTGATAATGTGTGTGTGGGGGAAATGGATCTACTTGT 2122
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US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14
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Query Match 17.1%; Score 558.6; DB 3; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;
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Db 2501 CTTACAGAGATCATTTGACATCAATGGAACAGTCACTGAATATAGCGTT 2551

RESULT 13
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-634-286A-14

Query Match 17.1%; Score 558.6; DB 4; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;

Qy 275 CCGGGTCCGAGAGCCGCTTCCGGAACCGACCTGGCGCACTGCTTCTACTCCGGCACCG 334
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Qy 335 TGAATGGCGATCCAGCTCGGCTGGCCCTCAGCTCTCGAGGGGGGTGGCGGCGCCT 394
Db 527 TGGACGCTAGTCCCGCTCTCTGGCTGTCTTGAACCTCTGTGGGGGTCTCGACGGCTTCT 586
Qy 395 TCTACCTGTCTGGGGAGGGGTATTTTCATCCAGCCGCTGCGCGCCGAGGAGCGCTCG 454
Db 587 TCGGGTTCAGACAGCGCGCTCACCTTAAGCCACTGCTGCGGAGACCTTGGGGGAGG 646
Qy 455 CCACCGCGCCCGCAGGAGGAGGAGCGCGCGCACCTACAGTTTCCACCTCTCTCGGCGGA 514
Db 647 AAGAAAGGGCGCTGTACGGGGATGGGTCCGACGGATCTTGCACGTCTACACCCGCG 706
Qy 515 ATCGGAGGGCGAGCGTAGGCGGCACTGTCGGGGTCTGTGAGAGAGAGCCCGCGCGACTG 574
Db 707 AGGGCTTCAGCTTCGAGGGCTCTGCGCGCGCTGCGCGCGCGAGTCCGAAACCCCGCGTCCAC 766
Qy 575 GGAAGCGGAGACCGAGAGCGAGGAGCGAGGGAGTGAAGGGGCTCAGT 634
Db 767 CGAGGGCCCAAGAGCATGCTCCCGGCGCAGCAACCCGAGCGGAGCGGAGCATGGCCT 826
Qy 635 GGTCTGCGCAGGAGCCCGGCACTGCAAGCGCTAGGACAGCCACACAGGA-----ACTGAA 688
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Qy 689 GCATAAGAAAGAGCGATTTGTGTCAGTCACTGCTATGTGGAACCATGTTGTGGCAG 748
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Qy 749 ACCAGTGCATGGCAGATTTCCAGCGAGTGGTCTTAAGAGCATTTACCTTCTACGTTGTTT 808
Db 947 ACAGCTCCATGGCGCGGTGTATGCGCGGGGCGCTTGCAGCATTTACCTGTGACCTGGCCT 1006
Qy 809 CGGTGGCAGCAGATTTGTACAAACACCCAGAGATTCGTAATTTCAAGTTAGCTGTGGTGG 868
Db 1007 CCATCGCAATAGGCTGTACAGCCATGTAGCATCGAGAACCAATCCGCTTGGCCGTGG 1066
Qy 869 TGAAGATCTTGGTCAATCCACGATGAACAGAGGGGCGGAGTGAACCTTCCATCTGCTGCC 928

Db 1067 TGAAGTGTGTGCTAGCGCAAGGACAAGAGCCTGGAAGTGAGCAAGAACGCTGCCA 1126
QY 929 TCACCTCTGGGAACTTTTGCACACTGGCAGACGACCAACCCACCCAGTACCGGGATG 988
Db 1127 CCACACTCAAGAACTTTTGAAGTGGCAGCACCAACCAACCCAGCTGGGAGATGCCATG 1186
QY 989 CAGAGCACTATGACACAGCAATTTCTTCCACAGACAGGACTTGTGTGGTCCCGACAT 1048
Db 1187 AGAGACATACGATGAGCTATCTCTGTCTCGGAGGATTTATGTGGCATCAATCA 1246
QY 1049 GTGATACTCTTGGGATGGCTGTGTGAACTGTGTGATCCGAGCAAGACTGCTCG 1108
Db 1247 GTGACACCTGGGAATGGCAGAGCTGTGGACCATATGTTCTCCAGAGCGACTGTGCTG 1306
QY 1109 TCATAGAGATGATGTTTACAAGCTGCTTCCACAGCCCATGAATTAGGCCGAGTGT 1168
Db 1307 TGAATTAAGACATGGCCTCCAGCAGCCTTCACTGTGGCTCAGGAATCGGACATTTAC 1366
QY 1169 TTAACATGCCATGATGATGAAAGCAGTGTGCCAGCCTTAATGTGTGAACCCAGGATT 1228
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QY 1289 GTGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1348
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Db 1607 AGTGAACCTGACATTTGGGCTGTAGTACTCCGTGTGTCCCGGCATGGATGTC--TGTG 1663
QY 1469 GCACCTTGTGTGTACCGGACCTCTGTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1528
Db 1664 CTCGCTGT 1723
QY 1529 CGTGGCGGATGCGACACGCTGTGTGAGAGGGAATGTTGATCAACGGCAAGTGTGTGA 1588
Db 1724 CTGGGTGGAAGGAGCGCTTGTGGAAGGGGAGATCTGCCCTGACAGGCAATGTGTGG 1783
QY 1589 ACAAACCCACAGAAAGCAATTTGTATACGCTTTTTCATGGAAGCTGGGGAATGTGGGGC 1648
Db 1784 ACAAACCAAGAAAATAATTAATCAACGCTCAAGCATGGCACTGGGATCTTGGGAT 1843
QY 1649 CTTGGGAGACTGTTCGAGAACGTGGGTGGAGGAGTCCAGTACAGTACGATGAGGGAATGTG 1708
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Db 2021 AGGCCAAAATGGCTATCACTGTGATGCAAAAAGGAGTCAAAATCTTTGTGGAATGGGTTC 2080
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QY 2189 GAGCCACCAACATCGAAGTGAACAGCGGAACCCAGAGGGATCCAGGAACAATGGCAGCT 2248
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QY 2249 TTCTTGGCCATCAAAAGCTGCTGATGGCACATATATTTTAAATGGTGACTACACTTTGTCCA 2308
Db 2441 ATTTAGCCCTGAAAAGAAAACCGTGAGTACCTTATCAATGGAAGTACATGATCTCCA 2500
QY 2309 CTTAGAGCAAGACATTTATGTACAAAGGTGTGTCTTGGAGTACAGCGCT 2359
Db 2501 CTTCAGAGACTATCATTTGACATCAATGGAACAGTCAATGAACTATAGCGGTT 2551

RESULT 14

US-10-247-685-14
; Sequence 14, Application US/10247685
; Patent No. 6753176

; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-10-247-685-14

Query Match 17.1%; Score 558.6; DB 4; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;

QY 275 CCGGTTCGAGAGCGCGCTTCGGAAACCGACTGGCGGACTGCTTCTACTCGGCACCG 334
Db 467 CAGGAGGGGGACGAGTGGCGCTGGCGCCACCGGAGCCACTGCTTCTATCGGGGACAG 526
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Db 527 TGGACGCTAGTCCCCGCTCTTGGCTGTCTTTGACCTCTGTGGGGTCTCGACGGTTCT 586
QY 395 TCTACTCTGTGGGGAGGCGTATTTTCATCCAGCGCTGCCCGCCGACGAGCGCTCG 454
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Db 707 AGGGCTTCAGCTTCAGGGCCCTGCGCGCGCGCAGCTGCGGAAACCCCGCGTCCACAC 766
QY 575 CGAAAGCGGAGACCCGAAGACGAGGAGCTGAGGGCGAGGAGCTGAGGGCGGCTCAGT 634

Db 767 CGGAGGCCACGAGCATGCTCCGGCGCACAGCAACCGAGCGGACGCGACGACTGCGCT 826
Qy 635 GGTGCGCGAGGACCGGCACTCAAGCGGTAGCAGACGCGCCACAGCA-----ACTGGAA 688
Db 827 CGAGCTCTTTGGACCAAGTCGCTCTCTCGCCCGCTGGGGCTCAGACCGCAGACGTGTGT 886
Qy 689 GCATAAGAAAGACGATTTGTGTCCAGTCACCGCTATGTGGAAACCATGTCTTGTGGCAG 748
Db 887 GCGCGCGCGCGCGCTCCATCTCCCGGGCCCGCCAGGTGGAGCTGCTTCTGTGGTGGCTG 946
Qy 749 ACAGTGTGATGGCAGAAATTCACGGCAGTGTCTAAAGCAATTAACCTTCTCACGCTGTGTTT 808
Db 947 ACAGTGTGATGGCAGAAATTCACGGCAGTGTCTAAAGCAATTAACCTTCTCACGCTGTGTTT 1006
Qy 809 CGGTGGCAGCGAGATTTGTAACAAACACCCAGCATTCTGTAATTCAGTTAGCTCTGGTGTGG 868
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Qy 1169 TTAACATGCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1228
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Qy 1469 GCACCTTGTGTGTACCGGACCTCTGTGTGGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1528
Db 1664 CTGCGCTGT 1723
Qy 1529 GTGGGCGGATGGCAGCAGCTGTGGAGAGGAAATGTTATCAACGGCAAGTGTGTGA 1588
Db 1724 CTGCGGTGGAGGAGCGCTTGTGGAAAGGGGAGAACTCTGCTCAGCGGCAAAATGTGTGG 1783
Qy 1589 ACRAAACCGACAGAAAGCATTTTATATAGCTTTTATAGCTTTTATAGCTTTTATAGCTTTTATAGCTTTT 1648
Db 1784 ACRAAACCGACAGAAAGCATTTTATATAGCTTTTATAGCTTTTATAGCTTTTATAGCTTTTATAGCTTTT 1843
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Db 1844 CTTGGGCGCAGTGTCTCGCTCATGTGGAGGAGGAGTGCAGTTTGTGCTTATCGTCACTGTA 1903

Qy 1709 ACAACCCAGTCCCAAGAAATGGAGGAAGTACTGTCAAGGCAAAACGAGTGGCTTACAGAT 1768
Db 1904 ATAACCTGCTCCAGAAACCAACGAGCGCTACTGTCAAGGAGAGGGCCATCTACCGCT 1963
Qy 1769 CTTGTAACCTTGGAGCTGTCCAGACAAATAATGGAAGAAACCTTTAGAGGAGAACATGTG 1828
Db 1964 CTTGCACTCTCATGCGCTGCCCCACC---AATGTAATCATTTTCTGTCATGAACAGTGTG 2020
Qy 1829 AAGCACACACAGATTTTCAAAAGCTTCTTTGGGAGTGGGCTGGGTGGAATGGATTTC 1888
Db 2021 AGGCCAAATAATGCTATCAGTCTGATGCAAAAGAGTCAAACTTTTGTGATGGTGTTC 2080
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Db 2081 CCAATATGCAAGTGTCTGCGCAGCGATGTGTGCAAGCTGACCTGCAGAGCCAAAGGCA 2140
Qy 1949 TTGGCTACTTCTTCGTTTTCAGCCCGCCAGAGTGTAGATGCTTCCATGTAGCCAGATT 2008
Db 2141 CTGGCTACTATGTGGTATTTTCTCAAAGGTGACCGATGGCATGAATGTAGGCCGTACA 2200
Qy 2009 CCACCTCTGCTGTGCAAGGACAGTGTGTAAGCTGTGTGATGCTGATCGCATCATAGACT 2068
Db 2201 GTAATTCGCTCTGCTCGGGGAAAGTGTGTGAAGTGTGTGAGCGCATCATTTGGCT 2260
Qy 2069 CCAAAAGAAAGTTTGTATAATGTGTGTTTTCGGGGGAAATGGATCTACTTGTAAAAAAA 2128
Db 2261 CAAAGCTGCAGTATGACAGTGTGGAGTATGTGGAGGAGCAACTCCAGCTGTACAAGA 2320
Qy 2129 TATCAGATCAGTTACTAGTGTGAAAACCTGGATATCATGATATCATCATCAATTTCAACTG 2188
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Db 2381 GGGCAACCCACATAAAGTTTCGACAGTTCAAAGCAAGACAGACTAGATTCACTGCTCT 2440
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Db 2501 CTTCAGAGACTATCATTTGACATCAATGGAACAGTCATGAACATATAGCGGTT 2551

RESULT 15

US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 3126
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3126)
; OTHER INFORMATION: repolysin (ADAM family of metalloprotease)
US-09-392-184-7

Query Match 16.7%; Score 544.2; DB 3; Length 3126;
Best Local Similarity 55.0%; Pred. No. 5e-117;
Matches 1413; Conservative 0; Mismatches 1023; Indels 135; Gaps 12;

175 CTCCGCTCAGCGCCTTTTACCAGCAGCTGGATCTGGAGCTGGGCCCGCAGCAGCTTT 234
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3116 CTTCACTTGTCCGCTTTCGGAAGGCTTCGTGCTGGCGCTGGCGCCGAGCAGCTTC 3057
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235 TTGGCGCCCGCTTTCAGCTTCAGAAAGTGGGGCGCAATCCGGTCCAGAGCGCGCTT 294
Db
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295 CCGGAAACCGACTTGGCGCACTTCTTACTCCGGCAGCGTGAATGGCGATCCAGCTCG 354
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Qy
355 GCTGCGCCCTCAGCCTCTCGAGGCGCTGCGCGCGCTTCTTACTGCTGGGGAGGCG 414
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715 AGTCACCGCTATGTGAAACCACTGTGTTGGCAGACCACTCGATGCGCAATTCACAGCG 774
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2630 GAGGCGGCTTCTGTGAGAGCGTGTGTTGGCGGATGCGTCCATGGCTTCTACGGG 2571
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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11539.238 Million cell updates/sec

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Perfect score: 3261

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Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3257	99.9	3261	11	US-09-989-687-1
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6	3160	96.9	4676	13	US-10-105-929-1
7	3158.4	96.9	4447	18	US-10-755-889-133
8	3157.4	96.8	4352	19	US-10-741-600-776
9	3157.4	96.8	4459	19	US-10-741-600-777
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11	3156.8	96.8	3889	19	US-10-667-281-1

12	3156.8	96.8	4459	17	US-10-159-563-192	Sequence 192, App
13	3156.8	96.8	4459	17	US-10-159-563-308	Sequence 308, App
14	3156.8	96.8	4760	10	US-09-971-4298-17	Sequence 17, Appl
15	3155.2	96.8	4309	16	US-10-210-120-57	Sequence 57, Appl
16	3139.2	96.3	4014	11	US-09-989-687-125	Sequence 125, Appl
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18	2131.6	65.4	2184	9	US-09-445-023A-2	Sequence 2, Appl1
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43	634.6	19.5	3711	18	US-10-283-975A-398	Sequence 398, App
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ALIGNMENTS

RESULT 1

US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
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; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (1)..(2853)
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; OTHER INFORMATION: May be any nucleic acid
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; Publication No. US2004002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
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US-09-989-687-1

Query Match 99.98; Score 3257; DB 11; Length 3261;
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Db 2641 CCAGCCAGCACCAGACCTTTGTGTCAGACCAATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGG 2700
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Db 2701 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Qy 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 2820
Db 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 2820
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Db 2821 ATAGACTTTTGCACAAATGGCAGAAATGCAATTAAGTGGTTTAAAGTGGTTAGCTTTGAGG 2880
Qy 2881 CAAAGCAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGGCTGGAGGGATCCAGCGT 2940
Db 2881 CAAAGCAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGGCTGGAGGGATCCAGCGT 2940
Qy 2941 ATCTTCCAGTAAACAGTGAAGGTGTATCAGTAAGTGGGATTAATGAGGGTGAATAGAA 3000
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Qy 3181 AAAAAAAGAGAGGGCGCGCTCTAGAGGATCCCTCGAGGGGCCCAAGCTTACGC 3240
Db 3181 AAAAAAAGAGAGGGCGCGCTCTAGAGGATCCCTCGAGGGGCCCAAGCTTACGC 3240
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RESULT 3

US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US20040265808A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Query Match 97.9%; Score 3192; DB 18; Length 3430;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 CTGCAAGCTTTTACCAGCAGCTGATCTGAGCTCGCGCCCGGGAACAAGGAGGAGGAGG 240
Db 418 CTGCAAGCTTTTACCAGCAGCTGATCTGAGCTCGCGCCCGGGAACAAGGAGGAGGAGG 477
Qy 241 CCGGCTTCACTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGAGCGCGCTTCCGGAA 300
Db 478 CCGGCTTCACTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGAGCGCGCTTCCGGAA 537
Qy 301 ACCGACTGGCGACTGCTTCTACTCCGGAACCGTGAATGGCGATCCAGCTGGCTGCC 360
Db 538 ACCGACTGGCGACTGCTTCTACTCCGGAACCGTGAATGGCGATCCAGCTGGCTGCC 597
Qy 361 GCCTCAGCTCTGCGAGGGCGTGGCGGCGCTTCTACCTGTGGGGAGGGGTATTTC 420
Db 598 GCCTCAGCTCTGCGAGGGCGTGGCGGCGCTTCTACCTGTGGGGAGGGGTATTTC 657
Qy 421 ATCCAGCGCTGCGCGCGCGCTCCAGAGCGCTCGCCACCGCCCGCCAGGGAGAGCGCG 480
Db 658 ATCCAGCGCTGCGCGCGCGCTCCAGAGCGCTCGCCACCGCCCGCCAGGGAGAGCGCG 717
Qy 481 CCGGCACTACTACAGTTTCACTCTTCCGCGGGAATCGGAGGGCGGAGGAGGAGGAGG 540
Db 718 CCGGCACTACTACAGTTTCACTCTTCCGCGGGAATCGGAGGGCGGAGGAGGAGGAGG 777
Qy 541 TCGGGGTGTGGAACGAGCGCGCGGCTGGGAAAGCGGAGCGGAGCGAGGAGGAGGAGG 600
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|||||
1078 ATTCTTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGNAACAGAG 1137
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QY CCTGCGACCTCGTACGATGCCAACCGGAGTGCAGTTTACATTTGGGAGGACTCCAAA 1440
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QY GGGAGTGGGCTGCGGTGGAATGGAATCCCAAGTACGCTGGGCTCTCAACCAAGACAGG 1920
Db GGGAGTGGGCTGCGGTGGAATGGAATCCCAAGTACGCTGGGCTCTCAACCAAGACAGG 2157
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QY TACACCTACTTTCGTAAGAGTGGGCGAATGTTCTAAGTCATCTGAATTCGGTTCGCAGAGA 2520
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QY GGAGTTGAATCATCAGAGTAACTGCCAGTTGCAAAATTTGATAGGATAGTTAGTGGGAT 3060
Db GGAGTTGAATCATCAGAGTAACTGCCAGTTGCAAAATTTGATAGGATAGTTAGTGGGAT 3297


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/ Terrett, Jonathan
/ Hasting, Gregg
/ TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Ratner & Prestia
/ STREET: Box 980
/ CITY: Valley Forge
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19482
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/757,450
/ FILING DATE: 15-Jan-2004
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/115,286
/ FILING DATE: 04-Apr-2002
/ APPLICATION NUMBER: 08/845,496
/ FILING DATE: <Unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Prestia, Paul P
/ REGISTRATION NUMBER: 23,031
/ REFERENCE/DOCKET NUMBER: GH-70000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-407-0700
/ TELEFAX: 610-407-0701
/ TELEX: 846169
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4014 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
/
/ US-10-757-450-1
/
/ Query Match 97.08; Score 3161.6; DB 18; Length 4014;
/ Best Local Similarity 99.78; Pred. No. 0;
/ Matches 3178; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
/
/ QY 1 ATGGGGAAACGGAGCGGGCTCCGGGCTCTCGGAGCTTTGGGCCCGCTACCCAGCTGCTG 60
/ DB 517 ATGGGGAACGGAGCGGGCTCCGGGCTCTCGGAGCTTTGGGCCCGCTACCCAGCTGCTG 576
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/ QY 61 CTGCTCCGCGCGCGCTACTGCGCGCTGTGCGACGCACTCGGGCGCCCTCGAGGAGGAC 120
/ DB 577 CTGCTCCGCGCGCGCTACTGCGCGCTGTGCGACGCACTCGGGCGCCCTCGAGGAGGAC 636
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/ QY 121 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGACACGGGACACGCGCTCCGC 180
/ DB 637 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGACACGGGACACGCGCTCCGC 696
/
/ QY 181 CTGACGCGCTTTGACACGAGCTGGATCTGAGCTGGCGCCCGGACAGCAGCTTTTGGCG 240
/ DB 697 CTGACGCGCTTTGACACGAGCTGGATCTGAGCTGGCGCCCGGACAGCAGCTTTTGGCG 756
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/ QY 241 CCGCGCTTACGCTCCAGAACTGGGCGCAAAATCCGGGTCGAGAGCGCGCTTCCGGAA 300
/ DB 757 CCGCGCTTACGCTCCAGAACTGGGCGCAAAATCCGGGTCGAGAGCGCGCTTCCGGAA 816
/
/ QY 301 ACCGACCTGGCGCACTGCTTACTCCGGCACTGATGCGATCCGAGCTCCGCTGCC 360
/ DB 817 ACCGACCTGGCGCACTGCTTACTCCGGCACTGATGCGATCCGAGCTCCGCTGCC 876
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/ QY 361 GCGCTCAGCTCTCGGAGGGGCTCGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTC 420
/ DB
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/ 877 GCCTCAGCCTCTGCGAGGGGCTGCGGGGCGCTTCTACTCTGCTGGGGAGGCGGTATTTC 936
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/ 1177 GCGTAGGACAGCCCAAGGAACTGGAAGCATGAAGAAAGAGCGATTTGTGTCAGTCAAC 1236
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/ DB
/ 1957 CACTGCGCTGATGAGCGCAGCAATGATGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2016
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Qy	1681	GGAGTCCAGTACACGATGAGGGAATGTGAACAACCCAGTCCCAAAGAAATGAGGGAAGTAC	1740
Db	2197	GGAGTCCAGTACACGATGAGGGAATGTGAACAACCCAGTCCCAAAGAAATGAGGGAAGTAC	2256
Qy	1741	TGTGMAAGCAACGAGTGGCGCTACAGATCCGTGTAAACCTTCAGGACCTGTCCAGACCAATAAT	1800
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Db	2857	GTCTTGAGGTACAGCGCTCCTCTCGGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTC	2916
Qy	2401	AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAA	2460
Db	2917	AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAA	2976
Qy	2461	TACACCTACTCTCGTAAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACTTTTTGAGCA	2520
Db	2977	TACACCTACTCTCGTAAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACTTTTTGAGCA	3036
Qy	2521	TGGGTCAATCAAGAGTGGGCGAATGTTCTAAGTCAATGTGAATTTGGGTTGGCAGAGAAGA	2580
Db	3037	TGGGTCAATCAAGAGTGGGCGAATGTTCTAAGTCAATGTGAATTTGGGTTGGCAGAGAAGA	3096

RESULT 6

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US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460) ... (3360)
; US-10-105-929-1

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Query Match				96.9%; Score 3160; DB 13; Length 4676;
Best Local Similarity				99.6%; Pred. No. 0;
Matches 3177; Conservative				0; Mismatches 11; Indels 1; Gaps 1;
QY	1	ATGGGAAACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCGTATCCAGCGTCTG	60	
DB	511	ATGGGAAACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCGTATCCAGCGTCTG	570	
QY	61	CTGCTCGCGCGCGCTACTTGGCCGTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGGAC	120	
DB	571	CTGCTCGCGCGCGCTACTTGGCCGTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGGAC	630	
QY	121	GAGGAGCTAGTGTGCGGAGCTGAGCGGCCCGGGACACGCGCCTCCGC	180	
DB	631	GAGGAGCTAGTGTGCGGAGCTGAGCGGCCCGGGACACGCGCCTCCGC	690	
QY	181	CTGACGCTTTGACACGACGCTGATCTGGAGCTGGGGCCCGACAGCAGCTTTTGGCG	240	
DB	691	CTGACGCTTTGACACGACGCTGATCTGGAGCTGGGGCCCGACAGCAGCTTTTGGCG	750	
QY	241	CCGGCTTTCACGCTCCAGACGCTGGGGCGCAATCCGGGTCCGAGACGCCCTTCCGGA	300	
DB	751	CCGGCTTTCACGCTCCAGACGCTGGGGCGCAATCCGGGTCCGAGACGCCCTTCCGGA	810	
QY	301	ACCGACTGGCGCACTGCTTACTCCGGCACCGTGAAATGGCGATCCAGCTCGGCTGCC	360	
DB	811	ACCGACTGGCGCACTGCTTACTCCGGCACCGTGAAATGGCGATCCAGCTCGGCTGCC	870	
QY	361	GCCTCAGCCTCTGCGAGGCGTGGCGGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC	420	
DB	871	GCCTCAGCCTCTGCGAGGCGTGGCGGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC	930	
QY	421	ATCAGCGCTGTCGCGCGCGCAGGCGCTCGCCACCGCCCGCCAGGGGAGAGCCG	480	
DB	931	ATCAGCGCTGTCGCGCGCGCAGGCGCTCGCCACCGCCCGCCAGGGGAGAGCCG	990	
QY	481	CCGGCACCACTACAGTTTCCACCTCTTGGCGGAAATCGGCGGGCGACGTAGCGGCACG	540	
DB	991	CCGGCACCACTACAGTTTCCACCTCTTGGCGGAAATCGGCGGGCGACGTAGCGGCACG	1050	
QY	541	TGCGGGTCTGTGACGACGAGCCCGGCCGACTGGGAAACGCGAGACCGAAGACGAGGAC	600	
DB	1051	TGCGGGTCTGTGACGACGAGCCCGGCCGACTGGGAAACGCGAGACCGAAGACGAGGAC	1110	
QY	601	GAGGACCTCAGCGCGAGGAGGCGCTCAGTGTGCGCGCAGGACCGCGCAGCTGCA	660	
DB	1111	GAGGACCTCAGCGCGAGGAGGCGCTCAGTGTGCGCGCAGGACCGCGCAGCTGCA	1170	
QY	661	GGCGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGCGATTTGTGCCAGTCA	720	
DB	1171	GGCGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGCGATTTGTGCCAGTCA	1230	
QY	721	CGCTATGTGAAACCAATGCTTGTGGACAGACAGTTCGATGGCGAATTCACGCGAGTGT	780	
DB	1231	CGCTATGTGAAACCAATGCTTGTGGACAGACAGTTCGATGGCGAATTCACGCGAGTGT	1290	
QY	781	CTAAGCATTAACCTCTCACTGTTTTCGGTGGCAGCAGATTTGTACAAACCCCGAC	840	
DB	1291	CTAAGCATTAACCTCTCACTGTTTTCGGTGGCAGCAGATTTGTACAAACCCCGAC	1350	
QY	841	ATTGCTAATTCAGTTAGCTGGTGTGGAAGATCTTGGTCATCCACGATGAACAGAG	900	
DB	1351	ATTGCTAATTCAGTTAGCTGGTGTGGAAGATCTTGGTCATCCACGATGAACAGAG	1410	
QY	901	GGGCGGAGTGACCTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGCACCTGGCAGAG	960	
DB	1411	GGGCGGAGTGACCTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGCACCTGGCAGAG	1470	
QY	961	CAGCAACCCACCCAGTGACCGGGATGACAGACATATGACACAGCAATTTCTTTTACC	1020	
DB	1471	CAGCAACCCACCCAGTGACCGGGATGACAGACATATGACACAGCAATTTCTTTTACC	1530	
QY	1021	AGACAGGACTTGTGGGTCCGACATGTGATCTCTGGGATGGGTGATGTGGAACT	1080	
1531	AGACAGGACTTGTGTGGGTCCGACATGTGATCTCTGGGATGGGTGATGTGGAACT	1590		
1081	GTGTGTGATCCGAGCAGAAAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTGCTTC	1140		
1591	GTGTGTGATCCGAGCAGAAAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTGCTTC	1650		
1141	ACCACAGCCCATGAATATAGGCCACGCTGTTTAAATCCCATGATGATGCAAAAGCAGTGT	1200		
1651	ACCACAGCCCATGAATATAGGCCACGCTGTTTAAATCCCATGATGATGCAAAAGCAGTGT	1710		
1201	GCAGGCTTAATGCTGTGAACCAAGGATTCGCCATGATGCGCTCAATGCTTTCCACCTG	1260		
1711	GCAGGCTTAATGCTGTGAACCAAGGATTCGCCATGATGCGCTCAATGCTTTCCACCTG	1770		
1261	GAACACAGCCAGCTTGTGCTCCTTCAGTGCCTACATGATTAACATCATTTCTGGATAAT	1320		
1771	GAACACAGCCAGCTTGTGCTCCTTCAGTGCCTACATGATTAACATCATTTCTGGATAAT	1830		
1321	GCTCATGGGGAATGTTTGTATGGACAAAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTC	1380		
1831	GCTCATGGGGAATGTTTGTATGGACAAAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTC	1890		
1381	CCTGGCACCTCGTACGATGCCAACCGGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1440		
1891	CCTGGCACCTCGTACGATGCCAACCGGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1950		
1441	CACTGCCCTGTATGACGCGCAGCATGTAGCACCTCTGTGTGTACCGGACCTCTGTGTGG	1500		
1951	CACTGCCCTGTATGACGCGCAGCATGTAGCACCTCTGTGTGTACCGGACCTCTGTGTGG	2010		
1501	GTGCTCGTGTCTCAAAACCAACCACTTCCGCTGGGCGGATGGCACACAGCTGTGGAGAGGG	1560		
2011	GTGCTCGTGTCTCAAAACCAACCACTTCCGCTGGGCGGATGGCACACAGCTGTGGAGAGGG	2070		
1561	AAATGCTGTATCAACCGGCAAGTGTGAAACAAACCGACAGAAAGCATTTTGTACGCT	1620		
2071	AAATGCTGTATCAACCGGCAAGTGTGAAACAAACCGACAGAAAGCATTTTGTACGCT	2130		
1621	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTTCGAGAACGTGCGGTGA	1680		
2131	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTTCGAGAACGTGCGGTGA	2190		
1681	GGAGTCCAGTACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAAGTAC	1740		
2191	GGAGTCCAGTACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAAGTAC	2250		
1741	TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTGGAGACTGTCCAGACAATTAAT	1800		
2251	TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTGGAGACTGTCCAGACAATTAAT	2310		
1801	GGAAACCTTTTAGAGGGAACAAATGTGAAGCACACAAAGCTTTTCAAAAGCTTCCTTT	1860		
2311	GGAAACCTTTTAGAGGGAACAAATGTGAAGCACACAAAGCTTTTCAAAAGCTTCCTTT	2370		
1861	GGAGTGGGCTCGCGTGGAAATGGAATCCCAAGTACGCTGGCGCTCCACAAAGGACAGG	1920		
2371	GGAGTGGGCTCGCGTGGAAATGGAATCCCAAGTACGCTGGCGCTCCACAAAGGACAGG	2430		
1921	TGCAAGCTCATCTGCCAAGCAAAAGGCAATGGCTACTTCTTCGTTTGGAGCCCAAGT	1980		
2431	TGCAAGCTCATCTGCCAAGCAAAAGGCAATGGCTACTTCTTCGTTTGGAGCCCAAGT	2490		
1981	GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTA	2040		
2491	GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTA	2550		
2041	AAAGCTGGTGTGATCGCATATAGACTCCAAAAAGAAAGTTTGAATAATGTGTGTTC	2100		
2551	AAAGCTGGTGTGATCGCATATAGACTCCAAAAAGAAAGTTTGAATAATGTGTGTTC	2610		
2101	GGGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCACAAACCTGGA	2160		

Db 2611 GGGGGAATGGATCTACTTTGTAATAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2670
Qy 2161 TATCATGATATCATACAAATTCCTACTGAGCCACCAACATCAAGTGAACAGCGGAC 2220
Db 2671 TATCATGATATCATCAAAATTCCTACTGAGCCACCAACATCAAGTGAACAGCGGAC 2730
Qy 2221 CAGAGGGGATCAGGAACAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCAATAT 2280
Db 2731 CAGAGGGGATCAGGAACAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCAATAT 2790
Qy 2281 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATATGATACAAAGTGT 2340
Db 2791 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATATGATACAAAGTGT 2850
Qy 2341 GTCTTGAGGTACAGCGGCTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCCTCTC 2400
Db 2851 GTCTTGAGGTACAGCGGCTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCCTCTC 2910
Qy 2401 AAAGAGCCCTTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATAAA 2460
Db 2911 AAAGAGCCCTTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATAAA 2970
Qy 2461 TACACTACTCTGTAAGAAGAAAGAAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
Db 2971 TACACTACTCTGTAAGAAGAAAGAAATCTTTCAATGCTATCCCACTTTTTCAGCA 3030
Qy 2521 TGGGTCAATGAGAGTGGGGCAATGTTCTAAGTCATGTAATTTGGTTGGCAGAGAGA 2580
Db 3031 TGGGTCAATGAGAGTGGGGCAATGTTCTAAGTCATGTAATTTGGTTGGCAGAGAGA 3090
Qy 2581 CTGGTAGAATCCGAGACATTAATGACAGCCTGCTTCGAGTGTGCAAGAAAGTGAAG 2640
Db 3091 CTGGTAGAATCCGAGACATTAATGACAGCCTGCTTCGAGTGTGCAAGAAAGTGAAG 3150
Qy 2641 CCAGCAGACACAGACCTTTGTGAGACCAATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 2700
Db 3151 CCAGCAGACACAGACCTTTGTGAGACCAATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 3210
Qy 2701 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAAAGCTGGAAGTGTCTGCC 2760
Db 3211 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAAAGCTGGAAGTGTCTGCC 3270
Qy 2761 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTT 2820
Db 3271 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTT 3330
Qy 2821 ATAGACTTTTGCACAAATGCGAGATGCGATTAGTGGTTTAAAGTGTGTAGCTTTGA-G 2879
Db 3331 ATAGACTTTTGCACAAATGCGAGATGCGATTAGTGGTTTAAAGTGTGTAGCTTTGAGG 3390
Qy 2880 GCAAGGCAAGTGAGAGGGCTGTGTGAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 2939
Db 3391 GCAAGGCAAGTGAGAGGGCTGTGTGAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 3450
Qy 2940 TATCTTGCAGTAACACAGTGAGGTGTATCAGTAAGGTGGGATTTATGGGGGTAGAGAA 2999
Db 3451 TATCTTGCAGTAACACAGTGAGGTGTATCAGTAAGGTGGGATTTATGGGGGTAGAGAA 3510
Qy 3000 AGGAGTTGAATCATCAGAGTAACTGCGAGTTGCAAAATTTGTATAGATAGTTAGTGAGGA 3059
Db 3511 AGGAGTTGAATCATCAGAGTAACTGCGAGTTGCAAAATTTGTATAGATAGTTAGTGAGGA 3570
Qy 3060 TTATTAACTCTGAGCAGTGATATAGCAATAAANCCCCGGGCATTATTATTATT 3119
Db 3571 TTATTAACTCTGAGCAGTGATATAGCAATAAANCCCCGGGCATTATTATTATT 3630
Qy 3120 CTTTGTGTACATCTATTACAGTTTGTAGAAAAACCAAGCAATTTGTCAAAAAAAGAAAA 3179
Db 3631 CTTTGTGTACATCTATTACAGTTTGTAGAAAAACCAAGCAATTTGTCAAAAAAAGTTAGAA 3690
Qy 3180 AAAAAAAA 3188
Db 3691 CTATTACAA 3699

RESULT 7

US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Query Match 96.9%; Score 3158.4; DB 18; Length 4447;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1 ATGGGGAACGGGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCCGTACCCACGCTGCTG 60
Db 294 ATGGGGAACGGGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCCGTACCCACGCTGCTG 353
Qy 61 CTGCTCGCGCGGCGCTACTGSCCGTGTGACGCACTCGGGCGCCCTCCGAGGAGAC 120
Db 354 CTGCTCGCGCGGCGCTACTGSCCGTGTGACGCACTCGGGCGCCCTCCGAGGAGAC 413
Qy 121 GAGGAGCTAGTGTGCTCCGAGCTGAGCGCGCCCGGACACGGAACCAACGCGCTCCGC 180
Db 414 GAGGAGCTAGTGTGCTCCGAGCTGAGCGCGCCCGGACACGGAACCAACGCGCTCCGC 473
Qy 181 CTGACAGCCTTTGACCAAGCAGCTGGATCTGAGCTGCGGCGCGACAGCAGCTTTTGGCG 240
Db 474 CTGACAGCCTTTGACCAAGCAGCTGGATCTGAGCTGCGGCGCGACAGCAGCTTTTGGCG 533
Qy 241 CCGGCTTTCAGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 300
Db 534 CCGGCTTTCAGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 593
Qy 301 ACCGACCTGGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
Db 594 ACCGACCTGGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 653
Qy 361 GCGCTCAGCCTCTGAGGGGTGCGGCGCTTTCTACTCTGCTGGGGAGGCGGTATTTTC 420
Db 654 GCGCTCAGCCTCTGAGGGGTGCGGCGCTTTCTACTCTGCTGGGGAGGCGGTATTTTC 713
Qy 421 ATCCAGCGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCGG 480
Db 714 ATCCAGCGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCGG 773
Qy 481 CCGGCAACCACTACAGTTCCACCTCTCTGGGGCGGAATCGGAGGGCGACGTTAGCGGCGACG 540
Db 774 CCGGCAACCACTACAGTTCCACCTCTCTGGGGCGGAATCGGAGGGCGACGTTAGCGGCGACG 833
Qy 541 TCGGGGTCTGTGAGACGAGCGCCGCGCGACTGGGAAGCGGAGACCGAAGACGAGGAC 600
Db 834 TCGGGGTCTGTGAGACGAGCGCCGCGCGACTGGGAAGCGGAGACCGAAGACGAGGAC 893
Qy 601 GAAGGAGCTGAGGGCGAGGACGGAAGGGCTCAGTGTGCTGCGCAGGACCCGCACTGCAA 660
Db 894 GAAGGAGCTGAGGGCGAGGACGGAAGGGCTCAGTGTGCTGCGCAGGACCCGCACTGCAA 953

QY	661	GGCGTAGGACAGCCACAGAACTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCAC	720
DB	954	GGGGTAGGACAGCCACAGAACTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCAC	1013
QY	721	CGCTATGTGGAAACCAATGCTTGTGGCAGACCAAGTCAGTGGCAGAAATTCACGGCAGTGGT	780
DB	1014	CGCTATGTGGAAACCAATGCTTGTGGCAGACCAAGTCAGTGGCAGAAATTCACGGCAGTGGT	1073
QY	781	CTTAAGCATTACCTCTCTCAGTTGTTTTCGGTGGCAGCCAGATTTGTACAAAACACCCAGC	840
DB	1074	CTTAAGCATTACCTCTCTCAGTTGTTTTCGGTGGCAGCCAGATTTGTACAAAACACCCAGC	1133
QY	841	ATTTCGTAATTCAGTTAGCCCTGGTGGTGGTGAAGATCTTGGTCACTCACGATGAACAGAAG	900
DB	1134	ATTTCGTAATTCAGTTAGCCCTGGTGGTGGTGAAGATCTTGGTCACTCACGATGAACAGAAG	1193
QY	901	GGGCCGGAAAGTAGCTTCCAAATGTGCCCTCACCTCTGGGGAACTTTTGGCAACTGGCAGAAG	960
DB	1194	GGGCCGGAAAGTAGCTTCCAAATGTGCCCTCACCTCTGGGGAACTTTTGGCAACTGGCAGAAG	1253
QY	961	CAGCAAAACCCACCCAGTACCGGGATGACAGACATATGACACAGCAATTTCTTTTTCACC	1020
DB	1254	CAGCAAAACCCACCCAGTACCGGGATGACAGACATATGACACAGCAATTTCTTTTTCACC	1313
QY	1021	AGACAGGACTTGTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAACT	1080
DB	1314	AGACAGGACTTGTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAACT	1373
QY	1081	GTGTGTATCCGAGCAGAAAGCTGCTCCGTCAATGAAAGATGATGGTTTAAAGCTGCGCTTC	1140
DB	1374	GTGTGTATCCGAGCAGAAAGCTGCTCCGTCAATGAAAGATGATGGTTTAAAGCTGCGCTTC	1433
QY	1141	ACCACAGCCCATGAATTAGCGCAGCTGTTTAAATGCCACATGATGATGATGACAGAGTGT	1200
DB	1434	ACCACAGCCCATGAATTAGCGCAGCTGTTTAAATGCCACATGATGATGATGACAGAGTGT	1493
QY	1201	GCCAGCCTTAATGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTG	1260
DB	1494	GCCAGCCTTAATGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTG	1553
QY	1261	GACCACAGCCAGCCTTGGTCTCCTTGCAAGTGCCTTACATGATTAATCATATTTCTGGATAAT	1320
DB	1554	GACCACAGCCAGCCTTGGTCTCCTTGCAAGTGCCTTACATGATTAATCATATTTCTGGATAAT	1613
QY	1321	GGTCAATGGGAATGTTTGTATGAGCAAGCTTCCAGATCCCATACAGTCCCGAGCGATCTC	1380
DB	1614	GGTCAATGGGAATGTTTGTATGAGCAAGCTTCCAGATCCCATACAGTCCCGAGCGATCTC	1673
QY	1381	CCTGGCACCTCGTACGATGCCAACCGCAGTGCAGTGTATACATTTGGGGAGGACTCCAAA	1440
DB	1674	CCTGGCACCTCGTACGATGCCAACCGCAGTGCAGTGTATACATTTGGGGAGGACTCCAAA	1733
QY	1441	CACCTGCCCTGATGAGCAGCAGACATGATGACCTTGTGGTGTATACCGGCACTCTGTGGGG	1500
DB	1734	CACCTGCCCTGATGAGCAGCAGACATGATGACCTTGTGGTGTATACCGGCACTCTGTGGGG	1793
QY	1501	GTGCTGTGTGTCAAAACCAACTTCCCGTGGCGGATGGCACCAGCTGTGGAGAGGG	1560
DB	1794	GTGCTGTGTGTCAAAACCAACTTCCCGTGGCGGATGGCACCAGCTGTGGAGAGGG	1853
QY	1561	AAATGTGTATCAACGGCAGTGTGAAACAAACCGACAGAAAGCAATTTGTATACGCCT	1620
DB	1854	AAATGTGTGTATCAACGGCAGTGTGAAACAAACCGACAGAAAGCAATTTGTATACGCCT	1913
QY	1621	TTTTCATGGAAGCTGGGGAATGTGGGGCTTTGGGGAGATGTTTCCAGAACTGTGGGTGA	1680
DB	1914	TTTTCATGGAAGCTGGGGAATGTGGGGCTTTGGGGAGATGTTTCCAGAACTGTGGGTGA	1973
QY	1681	GGAGTCCAGTACAGATGAGGAATGTGAACCCAGTCCCAAGATGAGGAGGAAGTAC	1740
DB	1974	GGAGTCCAGTACAGATGAGGAATGTGAACCCAGTCCCAAGATGAGGAGGAAGTAC	2033
QY	1741	TGTGAAGGCACACGATGCGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAAATAAT	1800

DB	2034	TGTGAAGGCACACGATGCGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAAATAAT	2093
QY	1801	GGAAACCTTTTAGAGAGGAAACAAATGCTGAAGCACACAAAGAGTTTCAAAGCTTCTCTTT	1860
DB	2094	GGAAACCTTTTAGAGAGGAAACAAATGCTGAAGCACACAAAGAGTTTCAAAGCTTCTCTTT	2153
QY	1861	GGAGTGGGCTCGCGTGGAAATGGATTTCCAAAGTACGCTGGGCTCTCACAAAGGACAGG	1920
DB	2154	GGAGTGGGCTCGCGTGGAAATGGATTTCCAAAGTACGCTGGGCTCTCACAAAGGACAGG	2213
QY	1921	TGCAAGCTCATCTGCCAAGCCAAAGCATTGGCTACTTCTTCTGTTTTGAGCCCAAGGTT	1980
DB	2214	TGCAAGCTCATCTGCCAAGCCAAAGCATTGGCTACTTCTTCTGTTTTGAGCCCAAGGTT	2273
QY	1981	GTAGATGGTACTTCCATGTAGCCAGATTTCCACCTCTGTCTGTGCAAGGACAGATGTGTA	2040
DB	2274	GTAGATGGTACTTCCATGTAGCCAGATTTCCACCTCTGTCTGTGCAAGGACAGATGTGTA	2333
QY	2041	AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAATGTGTGTTTGC	2100
DB	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAATGTGTGTTTGC	2393
QY	2101	GGGGAAATGGATCTACTTGTAAATAATCAGGATCAGTTACTAGTGAACCTGGA	2160
DB	2394	GGGGAAATGGATCTACTTGTAAATAATCAGGATCAGTTACTAGTGAACCTGGA	2453
QY	2161	TATCATGATATCATCAATTTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAAC	2220
DB	2454	TATCATGATATCATCAATTTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAAC	2513
QY	2221	CAGAGGGATCCAGGAACCAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT	2280
DB	2514	CAGAGGGATCCAGGAACCAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT	2573
QY	2281	ATTCTTAATGGTGACTACATTTGTCCACCTTAGCAAGACACATTTATGTAACAAAGTGT	2340
DB	2574	ATTCTTAATGGTGACTACATTTGTCCACCTTAGCAAGACACATTTATGTAACAAAGTGT	2633
QY	2341	GTCTTCAGGTACAGCGCTCTCTCGGCAATCGMAAGATTCGACGCTTTAGCCCTCTC	2400
DB	2634	GTCTTCAGGTACAGCGCTCTCTCGGCAATCGMAAGATTCGACGCTTTAGCCCTCTC	2693
QY	2401	AAAGAGCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAAT	2460
DB	2694	AAAGAGCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAAT	2753
QY	2461	TACACCTATCTTCTGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTCAGCA	2520
DB	2754	TACACCTATCTTCTGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTCAGCA	2813
QY	2521	TGGGTCAATTGAAGAGTGGGCGGAATGTTCTAAGTCAATGCAATTTGGGTGGCAGAGAAGA	2580
DB	2814	TGGGTCAATTGAAGAGTGGGCGGAATGTTCTAAGTCAATGCAATTTGGGTGGCAGAGAAGA	2873
QY	2581	CTGTGAGAAATGCCAGACATTAATGACAGCTGCTTCCGAGTGTGCAAAAGGAGTGAAG	2640
DB	2874	CTGTGAGAAATGCCAGACATTAATGACAGCTGCTTCCGAGTGTGCAAAAGGAGTGAAG	2933
QY	2641	CCAGCCAGCACAGACCTTGTGACAGCATTCTTCCCTGCCCGCCAGCTGGGGAGTGG	2700
DB	2934	CCAGCCAGCACAGACCTTGTGACAGCATTCTTCCCTGCCCGCCAGCTGGGGAGTGG	2993
QY	2701	TCATCATGTTCTAAGACCTGTGGAGGGTTTACAAAAAGAAAGCTTTGAAGTGTCTGTCC	2760
DB	2994	TCATCATGTTCTAAGACCTGTGGAGGGTTTACAAAAAGAAAGCTTTGAAGTGTCTGTCC	3053
QY	2761	CATGATGGAGGGTGTATCTCATGAGCTGTGATCTCTTTAAAGAAACCTTAACATTTTC	2820
DB	3054	CATGATGGAGGGTGTATCTCATGAGCTGTGATCTCTTTAAAGAAACCTTAACATTTTC	3113
QY	2821	ATAGACTTTTGCACAAATGGCAGAAATGAGTTAAGTGTGTTAAGTGTGTAGCTTTGA-G	2879

Db 3114 ATAGACTTTTGCACAAATGCGAGATGACAGTAAAGTGGTTTAAAGTGGTTAGCTTTGAGG 3173
QY 2880 GCAAGGCAAGTGAAGAGGCTGGTGCAGGGAAGCAAGAGGCTGGAGGATCCAGCG 2939
Db 3174 GCAAGGCAAGTGAAGAGGCTGGTGCAGGGAAGCAAGAGGCTGGAGGATCCAGCG 3233
QY 2940 TATCTTGCAGTAACCAAGTGAAGTATCAGTAAGTGGGATTAAGTGGGATAGATAAGAA 2999
Db 3234 TATCTTGCAGTAACCAAGTGAAGTATCAGTAAGTGGGATTAAGTGGGATAGATAAGAA 3293
QY 3000 AGAGTTGAATCATCAGAGTAACCTGCAAGTTCGCAAAATTTGATAGATAGTTAGTAGGA 3059
Db 3294 AGAGTTGAATCATCAGAGTAACCTGCAAGTTCGCAAAATTTGATAGATAGTTAGTAGGA 3353
QY 3060 TTATTAACCTCTGAGCAGTATAGCATTAATAAANCCCCGGCATTTATTATTATT 3119
Db 3354 TTATTAACCTCTGAGCAGTATAGCATTAATAAAGCCCCGGCATTTATTATTATT 3413
QY 3120 CTTTGTGTTACATCTATTACAGTTTAGAAAAACAAAGCAATTTGTCAAAAAA 3179
Db 3414 CTTTGTGTTACATCTATTACAGTTTAGAAAAACAAAGCAATTTGTCAAAAAA 3473
QY 3180 AAAAAAAA 3188
Db 3474 CTATTACAA 3482

RESULT 8

US-10-741-600-776
; Sequence 776, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 4352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4352)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-776

Query Match 96.8%; Score 3157.4; DB 19; Length 4352;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3169; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
QY 1 ATGGGGAACGCGAGCGGCTCCGGGCTCTCGAGCTTTGGGCCCGTACCACGCTGCTG 60
Db 513 ATGGGGAACGCGAGCGGCTCCGGGCTCTCGAGCTTTGGGCCCGTACCACGCTGCTG 572
QY 61 CTGCTCGCGCGCGGCTACTGCGCGTGTGCGAGCGCACTCGCGCGCCCTCCGAGAGGAC 120
Db 573 CTGCTCGCGCGCGGCTACTGCGCGTGTGCGAGCGCACTCGCGCGCCCTCCGAGAGGAC 632
QY 121 GAGGAGCTAGTGGTCCGAGCTGAGCGCGCCCGGAGCACGGACCCAGCGGCTCCGCG 180
Db 633 GAGGAGCTAGTGGTCCGAGCTGAGCGCGCCCGGAGCACGGACCCAGCGGCTCCGCG 692
QY 181 CTGCAAGCTTTGACCAAGCTGATCTGAGCTGCGGCGCGGAGCACAGCAGCTTTTGGCG 240
Db 693 CTGCAAGCTTTGACCAAGCTGATCTGAGCTGCGGCGCGGAGCACAGCAGCTTTTGGCG 752
QY 241 CCCGGCTTCAAGCTTCAAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGA 300
Db 753 CCCGGCTTCAAGCTTCAAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGA 812

QY 301 ACCGACCTGGCGCACTGCTTCTACTCCGSCACCCGTGAATGGGATCCAGCTCGGCTGCC 360
Db 813 ACCGACCTGGCGCACTGCTTCTACTCCGSCACCCGTGAATGGGATCCAGCTCGGCTGCC 872
QY 361 GCCCTCAGCCTCTCGAGGGGCTGCGCGGCTTCTACTCTGCTGGGGAGCGCTATTTTC 420
Db 873 GCCCTCAGCCTCTCGAGGGGCTGCGCGGCTTCTACTCTGCTGGGGAGCGCTATTTTC 932
QY 421 ATCCAGCGCTGCCCGCGCGAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCCG 480
Db 933 ATCCAGCGCTGCCCGCGCGAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCCG 992
QY 481 CCGGCACCACTACAGTTCACCTCTGCGGGGGAATCGSCAGGGGAGCTAGCGGCGCAG 540
Db 993 CCGGCACCACTACAGTTCACCTCTGCGGGGGAATCGSCAGGGGAGCTAGCGGCGCAG 1052
QY 541 TCGGGGCTCGTGAGCAGCAGCGCCCGCGCGACTGGGAAAGCGGAGACCGAAACAGCAGAC 600
Db 1053 TCGGGGCTSGTGAGCAGCAGCGCCCGCGCGACTGGGAAAGCGGAGACCGAAACAGCAGAC 1112
QY 601 GAAGGACTGAGGGCGAGGACGAAGGGCTCTAGTGGTTCGCCCGCAGGACCCGCGACTGCA 660
Db 1113 GAAGGACTGAGGGCGAGGACGAAGGGCTCTAGTGGTTCGCCCGCAGGACCCGCGACTGCA 1172
QY 661 GCGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGAGCGAATTTGTGCCAGTCA 720
Db 1173 GCGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGAGCGAATTTGTGCCAGTCA 1232
QY 721 CGTATGTGGAACCATGCTTGTGGCAGACCACTGATGGCAAGATTTCCAGCGAGTGT 780
Db 1233 CGTATGTGGAACCATGCTTGTGGCAGACCACTGATGGCAAGATTTCCAGCGAGTGT 1292
QY 781 CTAAAGCATTTACCTTCTCAGCTTTTCGTTGGCGAGCGCAGATTTGTACAAACACCCCGC 840
Db 1293 CTAAAGCATTTACCTTCTCAGCTTTTCGTTGGCGAGCGCAGATTTGTACAAACACCCCGC 1352
QY 841 ATTCTTAATTCAGTTAGCTGCTGCTGTTGAAGATCTTGTCTCATCAGCATCAACAGAG 900
Db 1353 ATTCTTAATTCAGTTAGCTGCTGCTGTTGAAGATCTTGTCTCATCAGCATCAACAGAG 1412
QY 901 GGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTCGGAACTTTTGAACCTGGCAGAG 960
Db 1413 GGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTCGGAACTTTTGAACCTGGCAGAG 1472
QY 961 CAGCAAAACCCAGTGAACCGGATGCGAGGACTATGACAGCAATTTCTTTTCCAC 1020
Db 1473 CAGCAAAACCCAGTGAACCGGATGCGAGGACTATGACAGCAATTTCTTTTCCAC 1532
QY 1021 AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGGAAC 1080
Db 1533 AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGGAAC 1592
QY 1081 GTGTGTATCCGAGCAGAACTGCTCCGTCTATAGAAGATGATGTTTCAAGCTGCTTTC 1140
Db 1593 GTGTGTATCCGAGCAGAACTGCTCCGTCTATAGAAGATGATGTTTCAAGCTGCTTTC 1652
QY 1141 ACCACAGCCATGAATTAAGGCACTGTTTAACTGACCATGATGATGATGATGATGAT 1200
Db 1653 ACCACAGCCATGAATTAAGGCACTGTTTAACTGACCATGATGATGATGATGATGAT 1712
QY 1201 GCCAGCCTTAATGTTGTAACCCAGGATTTCCACATGATGGGCTCAATGCTTTCCAACTG 1260
Db 1713 GCCAGCCTTAATGTTGTAACCCAGGATTTCCACATGATGGGCTCAATGCTTTCCAACTG 1772
QY 1261 GACCAAGCAGCCTTGGTCTCTTTCAGTGCCTACATGATTAATTAATTTCTGATAT 1320
Db 1773 GACCAAGCAGCCTTGGTCTCTTTCAGTGCCTACATGATTAATTAATTTCTGATAT 1832
QY 1321 GGTCTAGGGGATGTTTGTATGGAAGAGCTCAGATTCAGATCCATACAGCTCCAGCGCAT 1380
Db 1833 GGTCTAGGGGATGTTTGTATGGAAGAGCTCAGATTCAGATCCATACAGCTCCAGCGCAT 1892

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QY 1381 CTTGGCACTCGTACGATGCCAACCGCAGTGCAGTTTACATTTGGGGAGACTCCAAA 1440
Db 1893 CTTGGCACTCGTACGATGCCAACCGCAGTGCAGTTTACATTTGGGGAGACTCCAAA 1952
QY 1441 CACTGCCCTGATGAGCGACGACAATGTAGCACTTGTGTGTTGTTACCGGACCTCTGTGTGG 1500
Db 1953 CACTGCCCTGATGAGCGACGACAATGTAGCACTTGTGTGTTGTTACCGGACCTCTGTGTGG 2012
QY 1501 GTCTGGTGTGTCAAACCAACCACTTCCCGTGGCGGATGGCAGCTGTGTGAGAGGG 1560
Db 2013 GTCTGGTGTGTCAAACCAACCACTTCCCGTGGCGGATGGCAGCTGTGTGAGAGGG 2072
QY 1561 AAATGTGTATCAACCGCAGTGTGTGAAACAAACCGACAGAAAGCAATTTGTATGCGCCT 1620
Db 2073 AAATGTGTATCAACCGCAGTGTGTGAAACAAACCGACAGAAAGCAATTTGTATGCGCCT 2132
QY 1621 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 1680
Db 2133 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTTGGGGAGACTGTTCGAGAACGTGCGGTGGA 2192
QY 1681 GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC 1740
Db 2193 GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC 2252
QY 1741 TGTGAAGGCCAAAACGAGTGCCTACAGATCCTGTAAACCTTGAGGACTGTCCAGACAAATAAT 1800
Db 2253 TGTGAAGGCCAAAACGAGTGCCTACAGATCCTGTAAACCTTGAGGACTGTCCAGACAAATAAT 2312
QY 1801 GGAATAACCTTTAGAGAGGAACAAATGTGAAGGCAACAACGAGTTTTCAAAAGCTTCCTTTT 1860
Db 2313 GGAATAACCTTTAGAGAGGAACAAATGTGAAGGCAACAACGAGTTTTCAAAAGCTTCCTTTT 2372
QY 1861 GGGAGTGGGCTGGGTGGATGATGATTCACCAAGTACGCTGGCGCTCTACCAAGAGGACAGG 1920
Db 2373 GGGAGTGGGCTGGGTGGATGATGATTCACCAAGTACGCTGGCGCTCTACCAAGAGGACAGG 2432
QY 1921 TGCAGCTCATCTGCCAAGCAAGGCAATGGGCTACTTCTTCGTTTTGCGACCCCAAGGTT 1980
Db 2433 TGCAGCTCATCTGCCAAGCAAGGCAATGGGCTACTTCTTCGTTTTGCGACCCCAAGGTT 2492
QY 1981 GTAGATGGTACTCCATGATGCCAGATTCACACCTCTCTGTGTGTGCAAGGACAGTGTGTA 2040
Db 2493 GTAGATGGTACTCCATGATGCCAGATTCACACCTCTCTGTGTGTGCAAGGACAGTGTGTA 2552
QY 2041 AAAGCTGGTGTGATCCCATCATAGACTCCAAAGAAAGTTGATAAATGTGGTGTGTC 2100
Db 2553 AAAGCTGGTGTGATCCCATCATAGACTCCAAAGAAAGTTGATAAATGTGGTGTGTC 2612
QY 2101 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTCAAAACCTGGA 2160
Db 2613 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTCAAAACCTGGA 2672
QY 2161 TATCATGATATCATCAATTTCCAACCTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220
Db 2673 TATCATGATATCATCAATTTCCAACCTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2732
QY 2221 CAGAGGGATCCAGGAACATGGCAGCTTTCTGCCATCAAGCTGCTGATGGGCACATAT 2280
Db 2733 CAGAGGGATCCAGGAACATGGCAGCTTTCTGCCATCAAGCTGCTGATGGGCACATAT 2792
QY 2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGTACAAAGTGT 2340
Db 2793 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGTACAAAGTGT 2852
QY 2341 GTCTTGAGGTACAGCGCTCTCTGCGGCATTTGAAAGAAATTCGACGTTTTCAGCCCTCTC 2400
Db 2853 GTCTTGAGGTACAGCGCTCTCTGCGGCATTTGAAAGAAATTCGACGTTTTCAGCCCTCTC 2912
QY 2401 AAAGAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA 2460
Db 2913 AAAGAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA 2972
QY 2461 TACACCTACTTCGTAAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTTCAGCA 2520
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RESULT 9

US-10-741-600-777

; Sequence 777, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: C1001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 777

; LENGTH: 4459

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(4459)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

; METHODS OF DETECTION AND USES THEREOF

US-10-741-600-777

Query Match		96.8%;	Score 3157.4;	DB 19;	Length 4459;
Best Local Similarity		99.4%;	Pred. No. 0;		
Matches 3169;		Conservative 8;	Mismatches 11;	Indels 1;	Gaps 1;
QY	1	ATGGGGAACGCGGAGCGGCTCCGGGCTCTCGAGCTTTGGGCGCGTACCACGCTGCTG	60		
DB	294	ATGGGGAACGCGGAGCGGCTCCGGGCTCTCGAGCTTTGGGCGCGTACCACGCTGCTG	353		
QY	61	CTGCTCGCGCGCGCTACTGCGCGTCTCGGACGCACTCGGCGCGCCCTCCGAGAGGAC	120		
DB	354	CTGCTCGCGCGCGCTACTGCGCGTCTCGGACGCACTCGGCGCGCCCTCCGAGAGGAC	413		
QY	121	GAGGAGCTAGTGGTGGCGGAGCTGGAGCGCGCCCGGGACACGGGACCGCGCTCCGC	180		
DB	414	GAGGAGCTAGTGGTGGCGGAGCTGGAGCGCGCCCGGGACACGGGACCGCGCTCCGC	473		
QY	181	CTGCACGCTTTGACACGAGCTGGATCTGGAGCTGCGGCGCGACACGAGCTTTTGGCG	240		
DB	474	CTGCACGCTTTGACACGAGCTGGATCTGGAGCTGCGGCGCGACACGAGCTTTTGGCG	533		
QY	241	CCCGCTTCCAGCTCCAGAACTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGAA	300		
DB	534	CCCGCTTCCAGCTCCAGAACTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGAA	593		
QY	301	ACCGACCTGGCGCACTGCTTCTACTCCGCGACCGTGAATGGCGATCCGAGCTCGGCTGCC	360		
DB	594	ACCGACCTGGCGCACTGCTTCTACTCCGCGACCGTGAATGGCGATCCGAGCTCGGCTGCC	653		
QY	361	GGCCTCAGCTCTGCGAGGCGTGGCGCGCTTCTACTCTGGGGAGCGCTATTTC	420		
DB	654	GGCCTCAGCTCTGCGAGGCGTGGCGCGCTTCTACTCTGGGGAGCGCTATTTC	713		
QY	421	ATCCAGCGCTCCCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG	480		
DB	714	ATCCAGCGCTCCCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG	773		
QY	481	CGGGACCACTACAGTTCCACCTCTCGCGCGGATCCGCGAGGCGAGCTAGCGGCGACG	540		
DB	774	CGGGACCACTACAGTTCCACCTCTCGCGCGGATCCGCGAGGCGAGCTAGCGGCGACG	833		
QY	541	TGCGGGTCTGTCAGCAGCAGCGCGCGCTGCGGAAAGCGGAGCAGGAGCAGGAC	600		
DB	834	TGCGGGTCTGTCAGCAGCAGCGCGCGCTGCGGAAAGCGGAGCAGGAGCAGGAGC	893		
QY	601	GAAGGACTGAGGGCGAGGACGAGGCGCTCAGTGGTCCCGCAGGACCCGCGACTGCAA	660		
DB	894	GAAGGACTGAGGGCGAGGACGAGGCGCTCAGTGGTCCCGCAGGACCCGCGACTGCAA	953		
QY	661	GGCGTAGGACGCCACAGGAACCTGGAGCATAAGAAAGAGCGATTTGTCTCAGTCAC	720		
DB	954	GGCGTAGGACGCCACAGGAACCTGGAGCATAAGAAAGAGCGATTTGTCTCAGTCAC	1013		
QY	721	CGCTATGTGGAACCATGCTGTGGCAGACCACTGATGGCAGAAATTCACGCGCAGTGGT	780		
DB	1014	CGCTATGTGGAACCATGCTGTGGCAGACCACTGATGGCAGAAATTCACGCGCAGTGGT	1073		
QY	781	CTAAAGCACTTACCTTCTCACTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCCGAC	840		
DB	1074	CTAAAGCACTTACCTTCTCACTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCCGAC	1133		
QY	841	ATTCTGTAATTCAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAG	900		
DB	1134	ATTCTGTAATTCAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAG	1193		
QY	901	GGGCGGAGTGAACCTTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGAACCTGGCAGAG	960		
DB	1194	GGGCGGAGTGAACCTTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGAACCTGGCAGAG	1253		
QY	961	CAGCAACACCCACCGAGTACCGGGATGAGAGCACTATGACACAGCAATCTTTTCCACC	1020		
DB	1254	CAGCAACACCCACCGAGTACCGGGATGAGAGCACTATGACACAGCAATCTTTTCCACC	1313		

QY	1021	AGACAGGACTTGTGTGGTCCGAGACATGTGATACTCTTTGGGATGGCTGATGTGGAACCT	1080		
DB	1314	AGACAGGACTTGTGTGGTCCGAGACATGTGATACTCTTTGGGATGGCTGATGTGGAACCT	1373		
QY	1081	GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGAGATGATGGTTTACAAGCTGCTTC	1140		
DB	1374	GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGAGATGATGGTTTACAAGCTGCTTC	1433		
QY	1141	ACCAAGCCATGAAATAGGCCACCTGTTTAACTGACCAATGATGATGATGATGATGATGAT	1200		
DB	1434	ACCAAGCCATGAAATAGGCCACCTGTTTAACTGACCAATGATGATGATGATGATGATGAT	1493		
QY	1201	GCAGGCTTAAATGCTGTAACCAAGGATTTCCACATGATGGCGTCAATGCTTTCCACCTG	1260		
DB	1494	GCAGGCTTAAATGCTGTAACCAAGGATTTCCACATGATGGCGTCAATGCTTTCCACCTG	1553		
QY	1261	GACACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAATACATCATTTCTGATTAAT	1320		
DB	1554	GACACAGCCAGCTTGGTCTCTTTCAGTGCCTACATGATTAATACATCATTTCTGATTAAT	1613		
QY	1321	GGTCAATGGGGAATGTTTGAAGCAAGCTCAGAAATCCATAACAGCTCCAGGCGATCTC	1380		
DB	1614	GGTCAATGGGGAATGTTTGAAGCAAGCTCAGAAATCCATAACAGCTCCAGGCGATCTC	1673		
QY	1381	CCTGGCAGCTCGTACGATGCCAACCGCGAGTCCAGTTTACATTTGGGGAGGACTCCAAA	1440		
DB	1674	CCTGGCAGCTCGTACGATGCCAACCGCGAGTCCAGTTTACATTTGGGGAGGACTCCAAA	1733		
QY	1441	CACTCCCTGTATGTCAGCAGCAGCATGTAGCACCTTTGTGTGTATACCGGACCTCTGCTGG	1500		
DB	1734	CACTCCCTGTATGTCAGCAGCAGCATGTAGCACCTTTGTGTGTATACCGGACCTCTGCTGG	1793		
QY	1501	GTGCTGTGTGTCAAACCAAACCACTTCCGTCGGGCGGATGGCACAGCTGTGGAGAGG	1560		
DB	1794	GTGCTGTGTGTCAAACCAAACCACTTCCGTCGGGCGGATGGCACAGCTGTGGAGAGG	1853		
QY	1561	AAATGGTGTATCAACCGCAAGTGTGTGAACAAACCGGAGGAGCAATTTTATACGCTC	1620		
DB	1854	AAATGGTGTATCAACCGCAAGTGTGTGAACAAACCGGAGGAGCAATTTTATACGCTC	1913		
QY	1621	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTTGGGGAGACTGTTCGAGAACCTGCTGCTGA	1680		
DB	1914	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTTGGGGAGACTGTTCGAGAACCTGCTGCTGA	1973		
QY	1681	GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC	1740		
DB	1974	GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC	2033		
QY	1741	TGTGAAGGCAACAGTGGCTTACAGATCCCTGTAACTTGGAGCTGTCCAGACAAATAT	1800		
DB	2034	TGTGAAGGCAACAGTGGCTTACAGATCCCTGTAACTTGGAGCTGTCCAGACAAATAT	2093		
QY	1801	GGAAAACTTTTAGAGAGGAACTATGTGAAGCACAACACGAGTTTTCAAAAGCTTCTCTTT	1860		
DB	2094	GGAAAACTTTTAGAGAGGAACTATGTGAAGCACAACACGAGTTTTCAAAAGCTTCTCTTT	2153		
QY	1861	GGGAGTGGGCTGCGGTGGAAATGGAATCCCAAGTACGCTGGGCTCTCACAAAGGACAGG	1920		
DB	2154	GGGAGTGGGCTGCGGTGGAAATGGAATCCCAAGTACGCTGGGCTCTCACAAAGGACAGG	2213		
QY	1921	TGCAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTGTTTTCAGGCCCAAGGTT	1980		
DB	2214	TGCAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTGTTTTCAGGCCCAAGGTT	2273		
QY	1981	GTAGATGGTACTTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA	2040		
DB	2274	GTAGATGGTACTTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA	2333		
QY	2041	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAAGAAAGTTTGAATAATGTGGTGTTCG	2100		
DB	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAAGAAAGTTTGAATAATGTGGTGTTCG	2393		

QY 2101 GGGGGAATGGATCTACTTTGTAATAAATAATACAGATCAGTTACTAGTGCAAAACCTGGA 2160
DB 2394 GGGGGAATGGATCTACTTTGTAATAAATAATACAGATCAGTTACTAGTGCAAAACCTGGA 2453
QY 2161 TATCATGATATCATCAATTCCTCACTGGAGCCACCAATCGAAGTGAACAGCGGAC 2220
DB 2454 TATCATGATATCATCAATTCCTCACTGGAGCCACCAATCGAAGTGAACAGCGGAC 2513
QY 2221 CAGAGGGGATCCAGGAACATGCGAGCTTCTTGCCATCAAGCTGCTGATGCAATAT 2280
DB 2514 CAGAGGGGATCCAGGAACATGCGAGCTTCTTGCCATCAAGCTGCTGATGCAATAT 2573
QY 2281 ATTCTTAATGGTACTACACTTTGTCCACTTAGACCAAGACATATATGACAAAGTGT 2340
DB 2574 ATTCTTAATGGTACTACACTTTGTCCACTTAGACCAAGACATATATGACAAAGTGT 2633
QY 2341 GTCTTGAGGTACAGCGGCTCTCTGCGGCATTTGGAAGATTCGCGAGCTTTAGCCCTCTC 2400
DB 2634 GTCTTGAGGTACAGCGGCTCTCTGCGGCATTTGGAAGATTCGCGAGCTTTAGCCCTCTC 2693
QY 2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2460
DB 2694 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2753
QY 2461 TACACCTACTTCTGTAAGGAAGAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520
DB 2754 TACACCTACTTCTGTAAGGAAGAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2813
QY 2521 TGGGTCAATGAAGTGGGCGGAATGTTCTAAGTCATGTGAATGGTGGGTCGAGAGAAGA 2580
DB 2814 TGGGTCAATGAAGTGGGCGGAATGTTCTAAGTCATGTGAATGGTGGGTCGAGAGAAGA 2873
QY 2581 CTGTAGAAATGCCGAGACATTAATGACAGCTGCTTCCAGGTGTCARAAGGAAGTGAAG 2640
DB 2874 CTGTAGAAATGCCGAGACATTAATGACAGCTGCTTCCAGGTGTCARAAGGAAGTGAAG 2933
QY 2641 CCAGCCAGCACAGACCTTGTGAGACACATCCCTGCCCCAGTGGGAGGTGG 2700
DB 2934 CCAGCCAGCACAGACCTTGTGAGACACATCCCTGCCCCAGTGGGAGGTGG 2993
QY 2701 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAAAGAGCTTGAAGTGTCTGTCC 2760
DB 2994 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAAAGAGCTTGAAGTGTCTGTCC 3053
QY 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTTC 2820
DB 3054 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTTC 3113
QY 2821 ATAGACTTTTGCAATGGCAGATGCAATTAAGTGGTTTAAAGTGTGTTAGCTTTGA - G 2879
DB 3114 ATAGACTTTTGCAATGGCAGATGCAATTAAGTGGTTTAAAGTGTGTTAGCTTTGAAG 3173
QY 2880 GCAAGGCAAGTGAAGAGGGTGGTGCAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 2939
DB 3174 GCAAGGCAAGTGAAGAGGGTGGTGCAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 3233
QY 2940 TATCTCCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTTATGGGGCTAGTAGAAA 2999
DB 3234 TATCTCCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTTATGGGGCTAGTAGAAA 3293
QY 3000 AGGAGTTGAAATCATCAGAGTAAATCGCCAGTTGCAATTTGATAGGATAGTTAGTAGGA 3059
DB 3294 AGGAGTTGAAATCATCAGAGTAAATCGCCAGTTGCAATTTGATAGGATAGTTAGTAGGA 3353
QY 3060 TTATTAACTCTGAGCAGTGTATAGCATATAAANCCCCGGGCATTTATTATTATTATTT 3119
DB 3354 TTATTAACTCTGAGCAGTGTATAGCATATAAAGCCCCGGGCATTTATTATTATTATTT 3413
QY 3120 CTTTGTGTAATCTATTATCAAGTTTGAAGAAAACAAAGCAATTTGCAAAAAAAGAAAA 3179
DB 3414 CTTTGTGTAATCTATTATCAAGTTTGAAGAAAACAAAGCAATTTGCAAAAAAAGTTAGAA 3473
QY 3180 AAAAAAAA 3188

DB 3474 CTATTACAA 3482
RESULT 10
US-10-741-600-775
; Sequence 775, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 4658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)...(4658)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-3
US-10-741-600-775
Query Match 96.8%; Score 3157.4; DB 19; Length 4658;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3169; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
QY 1 ATGGGGAACGCGAGCGGGCTCCGGGTCTCGAGCTTTGGGCGCGTACCACGCTGCTG 60
DB 513 ATGGGGAACGCGAGCGGGCTCCGGGTCTCGAGCTTTGGGCGMTATCCACGCTGCTG 572
QY 61 CTGCTCGCGCGCGCTACTGCGCGTGTGCGACGCTCGGCGCCCTCCGAGGAGGAC 120
DB 573 CTGCTCGCGCGCGCTACTGCGCGTGTGCGACGCTCGGCGCCCTCCGAGGAGGAC 632
QY 121 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGAACACGCGGACACGCGCTCCGC 180
DB 633 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGAACACGCGGACACGCGCTCCGC 692
QY 181 CTGACGCGCTTTCACAGACGCTGAGATGAGAGCTGCGGCGCGACAGCAGCTTTTGCG 240
DB 693 CTGACGCGCTTTCACAGACGCTGAGATGAGAGCTGCGGCGCGACAGCAGCTTTTGCG 752
QY 241 CCGGCTTTCAGCTCCAGAACGTTGGGCGCAATCCGGGTCCGAGAGCGGCTTCCGGA 300
DB 753 CCGGCTTTCAGCTCCAGAACGTTGGGCGCAATCCGGGTCCGAGAGCGGCTTCCGGA 812
QY 301 ACCGACTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
DB 813 ACCGACTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 872
QY 361 GCCTCTCAGCTCTCGAGGGCGTGCAGCGCGCTTCTACTGCTGGGGAGGCGTATTTC 420
DB 873 GCCTCTCAGCTCTCGAGGGCGTGCAGCGCGCTTCTACTGCTGGGGAGGCGTATTTC 932
QY 421 ATCAGCGCTGCGCGCGCGCAGGAGCGCTGCGCACCGCGCGCCCGCAGGGAGAGCCG 480
DB 933 ATCAGCGCTGCGCGCGCGCAGGAGCGCTGCGCACCGCGCGCCCGCAGGGAGAGCCG 992
QY 481 CCGGCACTTACAGTTTCCACCTCTCGCGCGGAATCCGAGGGCGGACGCTAGGCGGACG 540
DB 993 CCGGCACTTACAGTTTCCACCTCTCGCGCGGAATCCGAGGGCGGACGCTAGGCGGACG 1052
QY 541 TCGGGGTCTGTGACGACGAGCGCCCGCGCTGCGGAAAGCGGAGACCGAAGACGAGAC 600
DB 1053 TCGGGGTCTGTGACGACGAGCGCCCGCGCTGCGGAAAGCGGAGACCGAAGACGAGAC 1112
QY 601 GAAGGAGCTGAGGCGGAGGACGAAGGCGCTCAGTGTGCTCGCGGAGGACCGCGGCTGCA 660

Db	1113	G A A G G G A C T G A G G G C G A G G A C G A A A G G G S C T C A G T G G T C G C G C A G G A C C C G G C A C T G C A A	1170
Qy	661	G G C G T A G A C A G C C C A C A G G A A C T G G A A G A C A T A A G A A A G A A G C A T T T G T G T C C A G T C A C	720
Db	1173	G G C G T A G A C A G C C C A C A G G A A C T G G A A G A C A T A A G A A A G A A G C A T T T G T G T C C A G T C A C	1232
Qy	721	C G T A T G T G G A A A C C A T G C T T T G T G G C A G A C C A G T C G A T G G C A G A A T T C C A C G G C A G T G G T	780
Db	1233	C G C T A T G T G G A A A C C A T G C T T T G T G G C A G A C C A G T C G A T G G C A G A A T T C C A C G G C A G T G G T	1292
Qy	781	C T A A G A C A T T A C T T C T C A C G T T G T T T C G G T G C A G C C A G A T T G T A C A A C A C C C C A G C	840
Db	1293	C T A A G A C A T T A C C T T C T C A C G T T G T T C G G T G C A G C C A G A T T G T A C A A C A C C C C A G C	1352
Qy	841	A T T C G T A A T T C A G T T A G C T G C T G G T G G T G A A G A T C T T G G T C A T C C A C A G A T G A A C A G A A G	900
Db	1353	A T T C G T A A T T C A G T T A G C T G C T G G T G G T G N A G A T C T T G G T C A T C C A G A T G A A C A G A A G	1412
Qy	901	G G G C C G G A A G T A C C T C C A A T G C T G C C C T C A C T C T G G G A A C T T T T G C A A C T G G C A G A A G	960
Db	1413	G G G C C G G A A G T A C C T C C A A T G C T G C C C T C A C T C T G C G G A A C T T T T G C A A C T G G C A G A A G	1472
Qy	961	C A G C A A A C C C A C C A G T A G A C C G G G A T G C A G A G A C A T A T A C A C A G A C A A T T C T T T T C A C C	1020
Db	1473	C A G C A A A C C C A C C A G T A G A C C G G G A T G C A G A G A C A T A T A C A C A G A C A A T T C T T T T C A C C	1532
Qy	1021	A G A C A G A C T T G T G G G T C C A C A C A T A T G A T A C T C T C G G A T G G C T G A T G T T G G A A C T	1080
Db	1533	A G A C A G A C T T G T G G G T C C A C A C A T A T G A T A C T C T T G G G A T G G C T G A N T T T G G A A C T	1592
Qy	1081	G T G T G T A T C C G A C A G A A G T G T C C G G T C A T A G A A G A T A T G T T T T A C A A G T G C C T T C	1140
Db	1593	G T G T G T A T C C G A C A G A A G T G T C C G G T C A T A G A A G A T A T G T T T T A C A A G T G C C T T C	1652
Qy	1141	A C C A C A G C C C A T A A T T A G G C C A C G T G T T T A A C A T G C C A C A T A T A T G A T G A A G C A G T G T	1200
Db	1653	A C C A C A G C C C A T A A T T A G G C C A C G T G T T T A A C A T G C C A C A T A T A T G A T G A A G C A G T G T	1712
Qy	1201	G C C A G C C T T A A T G T G T G A C C A G A A T T C C A C A T A T G A T G G C T C A A T G C T T T C C A A C C T G	1260
Db	1713	G C C A G C C T T A A T G T G T G A C C A G A A T T C C A C A T A T G A T G G C T C A A T G C T T T C C A A C C T G	1772
Qy	1261	G A C C A C A G C C A C C T T G G T C T C C T P T G C A G T G C C T A C A T G A T T A C A T C A T T T C T T G G A T A A T	1320
Db	1773	G A C C A C A G C C A C C T T G G T C T C C T P T G C A G T G C C T A C A T G A T T A C A T C A T T T C T T G G A T A A T	1832
Qy	1321	G G T C A T G G G G A A T G T T T G A T G G A C A G C C T C A G A A T C C C A T A C A G T C C C A G G C A T C T C	1380
Db	1833	G G T C A T G G G G A A T G T T T G A T G G A C A A G C C T C A G A A T C C C A T A C A G T C C C A G G C A T C T C	1892
Qy	1381	C C T G G C A C C T G T A C A T G C C A A C C G C A G T G C C A G T T T A C A T T T G G G G A G A C T C C A A A	1440
Db	1893	C C T G G C A C C T G T A C A T G C C A A C C G C A G T G C C A G T T T A C A T T T G G G G A G A C T C C A A A	1952
Qy	1441	C A C T G C C C T G A T G C A G C C A G C A C A T A T A G A C A C T T T G T G G T A C C G G C A C C T C T G T G G G	1500
Db	1953	C A C T G C C C Y A N T A G C C A G C A C A T A T A G A C A C T T T G T G G T A C C G G C A C C T C T G T G G G	2012
Qy	1501	G T G C T G T G T G T C A A A C C A A C A C T T C C G T G G G C G A T G C A C C A G C T G T G A G A A G G G	1560
Db	2013	G T G C T G T G T G T C A A A C C A A A C A C T T C C C G T G G G C G A T G G C A C C A G C T G T G A G A A G G G	2072
Qy	1561	A A A T G G T G T A T C A A C G G C A A G T G T G A A C A A A C C G A C A A A G C A A T T T T G A T A C G C C T	1620
Db	2073	A A A T G G T G T A T C A A C G G C A A G T G T G A A C A A A C C G A C A A A G C A A T T T T G A T A C G C C T	2132
Qy	1621	T T T C A T G G A A G C T G G G A A T G T G G G G C C T T T G G G G A C T G T T C G A A A C G T G C R G T G G A	1680
Db	2133	T T T C A T G G A A G C T G G G A A T G T G G G G C C T T T G G G G A C T G T T C G A A A C G T G C R G T G G A	2192
Qy	1681	G G A G T C C A G T A C A C A T G A G G A A T G T A C A A C C A A G C C A A G A T C C C A A A G A A T G A G G A A G T A C	1740
Db	2193	G G A G T C C A G T A C A C A T G A G G A A T G T A C A A C C A A G C C A A G A A T G A G G A A G T A C	2252

QY	1741	TGTGAAGCAAAACGAGTGC	CGCTACAGATCTGTAAACCTTGAGGACTGTGCAGACAATAAT	1800
DB	2253	TGTGAAGCAAAACGAGTGC	CGCTACAGATCTGTAAACCTTGAGGACTGTGCAGACAATAAT	2312
QY	1801	GGAAAAACCTTTAGAGAGGAAC	AAATGTAAGCAACAAACGAGTTTTCAAAAGCTTCCTTT	1860
DB	2313	GGAAAAACCTTTAGAGAGGAAC	AAATGTAAGCAACAAACGAGTTTTCAAAAGCTTCCTTT	2372
QY	1861	GGGAGTGGCGCTGCGGTGG	AAATGGAATCCCAAGTAGCGCTGGCGTCTCACAAAAGGACAGG	1920
DB	2373	GGGAGTGGCGCTGCGGTGG	AAATGGAATCCCAAGTAGCGCTGGCGTCTCACAAAAGGACAGG	2432
QY	1921	TGCAAGCTCATCTGCGCAAG	CCAAAGGCAATGGCTACTTCTTCGTTTGGCAGCCCAAGTTT	1980
DB	2433	TGCAAGCTCATCTGCGCAAG	CCAAAGGCAATGGCTACTTCTTCGTTTGGCAGCCCAAGTTT	2492
QY	1981	GTAGATGGTACTCCATGTAG	CCCAAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGA	2040
DB	2493	GTAGATGGTACTCCATGTAG	CCCAAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGA	2552
QY	2041	AAAGCTGGTTGTGATCGCAT	CATAGACTCCAAAAAGAAAGTTTGANAATGTGGTGTGCTTC	2100
DB	2553	AAAGCTGGTTGTGATCGCAT	CATAGACTCCAAAAAGAAAGTTTGANAATGTGGTGTGCTTC	2612
QY	2101	GGGGGAATGGATCTACTTGT	TAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGGA	2160
DB	2613	GGGGGAATGGATCTACTTGT	TAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGGA	2672
QY	2161	TATCATGATATCATCAAAAT	TCCAACTGGAGCCCAACAATCGAAGTGAAACAGCGGAAC	2220
DB	2673	TATCATGATATCATCAAAAT	TCCAACTGGAGCCCAACAATCGAAGTGAAACAGCGGAAC	2732
QY	2221	CAGAGGGATCCAGGAACAA	TGGCAGCTTTCTTGCCATCAAAAGCTGCTGATGCGCAATAT	2280
DB	2733	CAGAGGGATCCAGGAACAA	TGGCAGCTTTCTTGCCATCAAAAGCTGCTGATGCGCAATAT	2792
QY	2281	ATTCTTAATGGTGTACTAC	CTTTGTGCACCTTAGAGCAAGACATATGTACAAAGGTGTT	2340
DB	2793	ATTCTTAATGGTGTACTAC	CTTTGTGCACCTTAGAGCAAGACATATGTACAAAGGTGTT	2852
QY	2341	GTCCTTGAGGTACAGCGCT	CTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC	2400
DB	2853	GTCCTTGAGGTACAGCGCT	CTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC	2912
QY	2401	AAAGAGCCCTTGACATCTG	ACAGTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA	2460
DB	2913	AAAGAGCCCTTGACATCTG	ACAGTCTTACTGTGGGCAATGCCCTTCGACCTAAAATTAAA	2972
QY	2461	TACACCTACTTCGTPAAAG	AAGAAGGAATCTTTCAATGCTATTCGCCACTTTTTCAGCA	2520
DB	2973	TACACCTACTTCGTPAAAG	AAGAAGGAATCTTTCAATGCTATTCGCCACTTTTTCAGCA	3032
QY	2521	TGGGTCTATTGAAGAGTGG	GGCGAATGTTCTAAGTCTATGTCAATTTGGTTGGCAGAGAGA	2580
DB	3033	TGGGTCTATTGAAGAGTGG	GGCGAATGTTCTAAGTCTATGTCAATTTGGTTGGCAGAGAGA	3092
QY	2581	CTGCTAGAATGCCGAGACA	TATTAATGGACAGCCCTCTTCGAGTGTGCAAAAGGAAGTGAAG	2640
DB	3093	CTGCTAGAATGCCGAGACA	TATTAATGGACAGCCCTCTTCGAGTGTGCAAAAGGAAGTGAAG	3152
QY	2641	CCAGCCAGCACAGACCTTG	TCGCGAGCCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGG	2700
DB	3153	CCAGCCAGCACAGACCTTG	TCGCGAGCCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGG	3212
QY	2701	TCATCATGTTCTAAGACTGT	GGGAAGGGTTACAAAAAAGAAAGCTTTGAAGTGTCTGTCTCC	2760
DB	3213	TCATCATGTTCTAAGACTGT	GGGAAGGGTTACAAAAAAGAAAGCTTTGAAGTGTCTGTCTCC	3272
QY	2761	CATGATGGAGGGGTGTTAT	CTCATGAGAGCTGTGATCTCTTTTAAAGAAACCTAAACATTTTC	2820
DB	3273	CATGATGGAGGGGTGTTAT	CTCATGAGAGCTGTGATCTCTTTTAAAGAAACCTAAACATTTTC	3332

1321 GGTCTATGGGGAATGTTTGTATGACCAAGCCTCAGAATCCCATACAGCTCCAGCGCATCTC 1380
Db
1379 GGTCTATGGGGAATGTTTGTATGACCAAGCCTCAGAATCCCATACAGCTCCAGCGCATCTC 1438
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1381 CCTGGCACCTCGTAGATCCAAACCGGAGTGCAGTCTTACATTTTGGGAGGACTCCAAA 1440
Db
1439 CCTGGCACCTCGTAGATCCAAACCGGAGTGCAGTCTTACATTTTGGGAGGACTCCAAA 1498
Qy
1441 CACTGGCCCTGATGACGACGACATGTAGCACTTGTGTGTGTACCGGACCTCTGTGTGG 1500
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1499 CACTGGCCCTGATGACGACGACATGTAGCACTTGTGTGTGTACCGGACCTCTGTGTGG 1558
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1501 GTGCTGTGTGTCAAAACCAACACATTCCTGGTGGGCGGATGGCACGAGTGTGGGAAGG 1560
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1559 GTGCTGTGTGTCAAAACCAACACATTCCTGGTGGGCGGATGGCACGAGTGTGGGAAGG 1618
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1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACGACAGAAAGCATTTTGTATACGCT 1620
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1619 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACGACAGAAAGCATTTTGTATACGCT 1678
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1621 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGAGACTGTTCGAGAAACGTGGCGTGA 1680
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1679 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGAGACTGTTCGAGAAACGTGGCGTGA 1738
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1681 GGAGTCCAGTACACGATGAGGGAATGTGAACACCCAGTCCCAAGAAATGGAGGGAAGTAC 1740
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1739 GGAGTCCAGTACACGATGAGGGAATGTGAACACCCAGTCCCAAGAAATGGAGGGAAGTAC 1798
Qy
1741 TGTGAAGCAACACGAGTGGCTACAGATCCTGTAACTTTGAGGACTGTCCAGACAAATAT 1800
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1799 TGTGAAGCAACACGAGTGGCTACAGATCCTGTAACTTTGAGGACTGTCCAGACAAATAT 1858
Qy
1801 GGAATAACCTTTAGAGAGGAACAATGTGAAGCACACAGAGTTTCAAAGCTTCCCTTT 1860
Db
1859 GGAATAACCTTTAGAGAGGAACAATGTGAAGCACACAGAGTTTCAAAGCTTCCCTTT 1918
Qy
1861 GGGAGTGGCCCTGGCGTGAATGGATCCCAAGTAGCTGGCGTCTCCAAAGGACACAGG 1920
Db
1919 GGGAGTGGCCCTGGCGTGAATGGATCCCAAGTAGCTGGCGTCTCCAAAGGACACAGG 1978
Qy
1921 TGCAAGCTCATCTGCCAAGCAAGGCAATGGCTACTTCTCGTTTTCAGGCCCAAGGTT 1980
Db
1979 TGCAAGCTCATCTGCCAAGCAAGGCAATGGCTACTTCTCGTTTTCAGGCCCAAGGTT 2038
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2039 GTAGATGTGTCTCATGTAGCCAGATTCCACTCTGTCTGTGTGTGAAGGACAGTGTGTA 2098
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2041 AAAGCTGGTGTGTGATCGCATCATAGACTCCAAAAGAGTTTGTATAATGTGGTGTTCG 2100
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2101 GGGGGAATGGATCTACTTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2160
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2159 GGGGGAATGGATCTACTTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2218
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2161 TATCATGATATCATCAAAATTCAACTGGAGGCCAACATCGAAAGTGAACAGCGGAAC 2220
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2219 TATCATGATATCATCAAAATTCAACTGGAGGCCAACATCGAAAGTGAACAGCGGAAC 2278
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2221 CAGAGGGATCAGGAACAATGGAGCTTTCTTGGCATCAAGAGCTGCTGATGGCACATAT 2280
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2281 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATTTATGACAAAGTGT 2340
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2339 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATTTATGACAAAGTGT 2398
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2341 GTCTTGAGGTACAGCGGCTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCCCTCTC 2400
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Qy
2461 TACACCTACTTCTGTAAAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
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2521 TGGGTCAATGAAGAGTGGGCGAATGTTCTAAGTCAATGTGAATGGTGGGCGAGAGA 2580
Db
2579 TGGGTCAATGAAGAGTGGGCGAATGTTCTAAGTCAATGTGAATGGTGGGCGAGAGA 2638
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2581 CTGGTAGAATGCCGAGACATTAATGACACAGCTGCTCCGAGTGTGCAAGCAAGTGAAG 2640
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2639 CTGGTAGAATGCCGAGACATTAATGACACAGCTGCTCCGAGTGTGCAAGCAAGTGAAG 2698
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2641 CCAGCAGCACAGACCTTGTGTGCAGACCATCCCTGCCCCAGCTGGCGGAGTGG 2700
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2699 CCAGCAGCACAGACCTTGTGTGCAGACCATCCCTGCCCCAGCTGGCGGAGTGG 2758
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Db
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Qy
2761 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTT 2820
Db
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Qy
2821 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGA-G 2879
Db
2879 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGAGG 2938
Qy
2880 GCAAGGCAAGTGAAGAGGCTGTGCAAGGAAGCAAGAGCTTGGAGGATCCAGCG 2939
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3000 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTTGCAGAAATTTGATAGGATAGTTAGTGA 3059
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3059 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTTGCAGAAATTTGATAGGATAGTTAGTGA 3118
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3060 TTATTAACTCTGACAGAGTATATAGCATATAAANCCCCGGGCATTATTATTATTTT 3119
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3120 CTTTTTTTACATCTATTACAGTTTGTAGAAAAACAAAGCAATTTGCAAAAAAAGTTAGAA 3179
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3179 CTTTTTTTACATCTATTACAGTTTGTAGAAAAACAAAGCAATTTGCAAAAAAAGTTAGAA 3238
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3180 AAAAAAAA 3188
Db
3239 CTATTACAA 3247

RESULT 12
US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; CURRENT FILING DATE: 2002-12-09
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-04-25

; NUMBER OF SEQ ID NOS: 444									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 192									
; LENGTH: 4459									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-159-563-192									
Query Match									
Best Local Similarity 96.8%; Score 3156.8; DB 17; Length 4459;									
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;									
QY	1	ATGGGNAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCCGTACCCAGCTGCTG	60						
DB	294	ATGGGNAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCCGTACCCAGCTGCTG	353						
QY	61	CTGCTCGCGCGCGCTACTTGGCCGTGTGGAAGCACTGGGGCGCCCTCCCGAGGAGGAC	120						
DB	354	CTGCTCGCGCGCGCTACTTGGCCGTGTGGAAGCACTGGGGCGCCCTCCCGAGGAGGAC	413						
QY	121	GAGGAGTAGTGTGGCGGAGCTGGAGCGGCCCGGGACACGGGACCGGCGCTCCGC	180						
DB	414	GAGGAGTAGTGTGGCGGAGCTGGAGCGGCCCGGGACACGGGACCGGCGCTCCGC	473						
QY	181	CTCAGCGCTTTGACAGCAGCTGGATCTGGAGCTGGCGCCCGACAGCAGCTTTTGGCG	240						
DB	474	CTGCAAGCTTTGACAGCAGCTGGATCTGGAGCTGGCGCCCGACAGCAGCTTTTGGCG	533						
QY	241	CCGGCTTCAAGCTCCAGAAAGTGGGGCGAAATCCGGGTCGAGACGCGCTTCCGGAA	300						
DB	534	CCGGCTTCAAGCTCCAGAAAGTGGGGCGAAATCCGGGTCGAGACGCGCTTCCGGAA	593						
QY	301	ACGAGCTGGCGCACTGCTTCTACTCGGCACCGTGAGTGGCGATCCAGCTCGGCTGCC	360						
DB	594	ACGAGCTGGCGCACTGCTTCTACTCGGCACCGTGAGTGGCGATCCAGCTCGGCTGCC	653						
QY	361	GCCTCAGCTCTGCGAGGCGCTGCGGGCGCTTCTACCTGTGGGGAGGCGTATTTTC	420						
DB	654	GCCTCAGCTCTGCGAGGCGCTGCGGGCGCTTCTACCTGTGGGGAGGCGTATTTTC	713						
QY	421	ATCCAGCGCTGCGCGCGCAGCGCGCTCGCCACCGCGCCCGCAGGGGAGAGCCG	480						
DB	714	ATCCAGCGCTGCGCGCGCAGCGCGCTCGCCACCGCGCCCGCAGGGGAGAGCCG	773						
QY	481	CCGGCACCCTACAGTTCCACTCTCTCGGGGGAATCGGCAGGGCGAGCTAGCGGCACG	540						
DB	774	CCGGCACCCTACAGTTCCACTCTCTCGGGGGAATCGGCAGGGCGAGCTAGCGGCACG	833						
QY	541	TGCGGGTCTGGACGACGAGCCCGCGCTGCGGAAAGCGGAGCCGAGACCGAGGAC	600						
DB	834	TGCGGGTCTGGACGACGAGCCCGCGCTGCGGAAAGCGGAGCCGAGGACCGAGGAC	893						
QY	601	GAAGGGAAGTGAAGGCGAGGAGGCGCTCAGTGGTCGCGCAGGACCCGGCAGTGCAA	660						
DB	894	GAAGGGAAGTGAAGGCGAGGAGGCGCTCAGTGGTCGCGCAGGACCCGGCAGTGCAA	953						
QY	661	GGGTAGGACAGCCCAAGAACTGGAAAGCAATAGAAAGAGCGATTGTCTCAGTCAAC	720						
DB	954	GGGTAGGACAGCCCAAGAACTGGAAAGCAATAGAAAGAGCGATTGTCTCAGTCAAC	1013						
QY	721	CGCTATCTGGAACCATCTGTGGCAGACAGCTGATGGCAGAAATCCACGGCAGTGT	780						
DB	1014	CGCTATCTGGAACCATCTGTGGCAGACAGCTGATGGCAGAAATCCACGGCAGTGT	1073						
QY	781	CTAAGCAATTAACCTTCTCAGCTTGTTCGGTGGCAGCGAGATTGTACAAACCCCGAGC	840						
DB	1074	CTAAGCAATTAACCTTCTCAGCTTGTTCGGTGGCAGCGAGATTGTACAAACCCCGAGC	1133						
QY	841	ATTGTAATTAACCTTGTGGTGGTGAAGATCTTGTGTCATCTCAGATGAACAGAG	900						
DB	1134	ATTGTAATTAACCTTGTGGTGGTGAAGATCTTGTGTCATCTCAGATGAACAGAG	1193						
QY	901	GGGCGGAGTAGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTCAACTGSCAGAAG	960						
DB	1194	GGGCGGAGTAGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTCAACTGSCAGAAG	1253						
QY	961	CAGCAACAACCCAGTGAACCGGATGAGAGCACTATGACACAGCAATTTCTTTTCAAC	1020						
DB	1254	CAGCAACAACCCAGTGAACCGGATGAGAGCACTATGACACAGCAATTTCTTTTCAAC	1313						
QY	1021	AGACAGGACTTGTGTGGTCCAGACATGTGATACTTTTGGGATGCTGATGTGGAAT	1080						
DB	1314	AGACAGGACTTGTGTGGTCCAGACATGTGATACTTTTGGGATGCTGATGTGGAAT	1373						
QY	1081	GTGTGTGATCCAGACAGAGCTGCTCCGTCATAGAGATGATGGTTTCAAGTCGCTTC	1140						
DB	1374	GTGTGTGATCCAGACAGAGCTGCTCCGTCATAGAGATGATGGTTTCAAGTCGCTTC	1433						
QY	1141	ACCACAGCCATGAATTAGGCCACAGTGTAAATGCCACATGATGATGATGATGATGAT	1200						
DB	1434	ACCACAGCCATGAATTAGGCCACAGTGTAAATGCCACATGATGATGATGATGATGAT	1493						
QY	1201	GCCAGCTTAAATGGTGTGAACCAAGGATCCCAATGATGCGCTCAATGCTTTTCCAACTG	1260						
DB	1494	GCCAGCTTAAATGGTGTGAACCAAGGATCCCAATGATGCGCTCAATGCTTTTCCAACTG	1553						
QY	1261	GACACAGCCAGCTTGGTCTCTTGCAGTGCCTACATGATGATGATGATGATGATGAT	1320						
DB	1554	GACACAGCCAGCTTGGTCTCTTGCAGTGCCTACATGATGATGATGATGATGATGAT	1613						
QY	1321	GGTCAATGGGGAATGTTGATGACAAAGCTCCAGAAATCCCATACAGCTCCAGCGATCTC	1380						
DB	1614	GGTCAATGGGGAATGTTGATGACAAAGCTCCAGAAATCCCATACAGCTCCAGCGATCTC	1673						
QY	1381	CTTGGCACCTCTGATCGATGCCAACCGGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1440						
DB	1674	CTTGGCACCTCTGATCGATGCCAACCGGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1733						
QY	1441	CACTGCGCTGATGACGACGACATGTAGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500						
DB	1734	CACTGCGCGCTGATGACGACGACATGTAGCACTTGTGTGTGTGTGTGTGTGTGTGTGT	1793						
QY	1501	GTGCTGGTGTGTCACCAACCAACTTCCCGTGGGCGGATGGCACAGCTGTGGAGAGGG	1560						
DB	1794	GTGCTGGTGTGTCACCAACCAACTTCCCGTGGGCGGATGGCACAGCTGTGGAGAGGG	1853						
QY	1561	AAATGTGTATCAACCGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTGTATAGCCT	1620						
DB	1854	AAATGTGTATCAACCGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTGTATAGCCT	1913						
QY	1621	TTTCAATGGAAGCTGGGGGAATGTGGGGCGCTTGGGGAGACTGTTCGAGAACGTGGGTGA	1680						
DB	1914	TTTCAATGGAAGCTGGGGGAATGTGGGGCGCTTGGGGAGACTGTTCGAGAACGTGGGTGA	1973						
QY	1681	GGAGTCCAGTACACGATGAGGGAATGTGAACCAACCGAGTCCCAAGAAATGAGGAGAGTAC	1740						
DB	1974	GGAGTCCAGTACACGATGAGGGAATGTGAACCAACCGAGTCCCAAGAAATGAGGAGAGTAC	2033						
QY	1741	TGTGAAGGCAACACGATGCGCTACAGATCTGTAAACCTTGAGGACTGTTCAGACCAATAT	1800						
DB	2034	TGTGAAGGCAACACGATGCGCTACAGATCTGTAAACCTTGAGGACTGTTCAGACCAATAT	2093						
QY	1801	GGAAAAACCTTTTAGAGAGGAACAAATGTGAAGCAACAACCGAGTTTCAAAGCTTCCTTT	1860						
DB	2094	GGAAAAACCTTTTAGAGAGGAACAAATGTGAAGCAACAACCGAGTTTCAAAGCTTCCTTT	2153						
QY	1861	GGAGTGGGCTCGGGTGGAAATGGAATCCCAAGTACGCTGCGCTCTCACCAGGACAGG	1920						
DB	2154	GGAGTGGGCTCGGGTGGAAATGGAATCCCAAGTACGCTGCGCTCTCACCAGGACAGG	2213						
QY	1921	TGCAAGCTCATCTGCCAAGCAAAAGCAATTTGGTACTTCTTCTGTTTGGAGCCCAAGTT	1980						
DB	2214	TGCAAGCTCATCTGCCAAGCAAAAGCAATTTGGTACTTCTTCTGTTTGGAGCCCAAGTT	2273						
QY	1981	GTAGATGGTATCCATGTAGCCAGGATTCACCTCTCTGTGTGTGTGTGTGTGTGTGTGT	2040						

Df	2274	GTAGATGGTACTCCATGTAGCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTA	2333
QY	2041	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAGAGTTTGATTAATATGCTGTTC	2100
Df	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAGAGTTTGATTAATATGCTGTTC	2393
QY	2101	GGGGAAATGGATCTACTTTGTAATAAATATCAGGATCAGTTACTAGTGCATAAATCCTGGA	2160
Df	2394	GGGGAAATGGATCTACTTTGTAATAAATATCAGGATCAGTTACTAGTGCATAAATCCTGGA	2453
QY	2161	TATCATGATATCATCAAAATCCAACTGGAGCCACCAATCAAGAGTGAACAGCGGAAC	2220
Df	2454	TATCATGATATCATCAAAATCCAACTGGAGCCACCAATCAAGAGTGAACAGCGGAAC	2513
QY	2221	CAGAGGGATCAGGACATGGCAGCTTCTTGCCATCAAGAGCTGCTGATGGCAGATAT	2280
Df	2514	CAGAGGGATCAGGACATGGCAGCTTCTTGCCATCAAGAGCTGCTGATGGCAGATAT	2573
QY	2281	ATTCTTAATGGTGACTACACTTTGTCCACTTTAGAGCAAGACATATGTACAAAGGTGT	2340
Df	2574	ATTCTTAATGGTGACTACACTTTGTCCACTTTAGAGCAAGACATATGTACAAAGGTGT	2633
QY	2341	GTCTTGAGGTACAGCGGTCTCTCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC	2400
Df	2634	GTCTTGAGGTACAGCGGTCTCTCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC	2693
QY	2401	AAAGAGCCCTTGACCATCCAGCTTCTTACTGTGGCAATGCCCTTCGACCTTAATAA	2460
Df	2694	AAAGAGCCCTTGACCATCCAGCTTCTTACTGTGGCAATGCCCTTCGACCTTAATAA	2753
QY	2461	TACACTACTCTGTAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA	2520
Df	2754	TACACTACTCTGTAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA	2813
QY	2521	TGGGTCAATGAAGAGTGGGCGAATGTTCTAAGTCAATGATGTAATGGTGGCAGAGA	2580
Df	2814	TGGGTCAATGAAGAGTGGGCGAATGTTCTAAGTCAATGATGTAATGGTGGCAGAGA	2873
QY	2581	CTGTTAGATCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAGGAAGTGAAG	2640
Df	2874	CTGTTAGATCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAGGAAGTGAAG	2933
QY	2641	CCAGCCAGCACAGACCTTTGTGCAGACCATCCCTGCCCTGCGAGCTGGGGAGTGG	2700
Df	2934	CCAGCCAGCACAGACCTTTGTGCAGACCATCCCTGCCCTGCGAGCTGGGGAGTGG	2993
QY	2701	TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC	2760
Df	2994	TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC	3053
QY	2761	CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAGAAACCTTAACATTTTC	2820
Df	3054	CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAGAAACCTTAACATTTTC	3113
QY	2821	ATAGACTTTTGCACAAATGGCAGAAATGAGTGAAGTGTGTTAAGTGTGTAGCTTTGA	2879
Df	3114	ATAGACTTTTGCACAAATGGCAGAAATGAGTGAAGTGTGTTAAGTGTGTAGCTTTGA	3173
QY	2880	GCAAGCAAGTGAAGAGGGTGTGTGAGGAAAGCAAGAGAGTGTGAGGATCCAGCG	2939
Df	3174	GCAAGCAAGTGAAGAGGGTGTGTGAGGAAAGCAAGAGAGTGTGAGGATCCAGCG	3233
QY	2940	TATCTTGCAGTAAACAGTGGTGTATCAGTAAGTGGGATTTATGGGGTATAGAGAA	2999
Df	3234	TATCTTGCAGTAAACAGTGGTGTATCAGTAAGTGGGATTTATGGGGTATAGAGAA	3293
QY	3000	AGGAGTTGAATCATCAGAGTAACTCCAGTTTGCATAATTTGATAGGATAGTTAGTGA	3059
Df	3294	AGGAGTTGAATCATCAGAGTAACTCCAGTTTGCATAATTTGATAGGATAGTTAGTGA	3353
QY	3060	TTATTAACTCTGAGCAGTATAGCATAATAAANCCCCGGGCAATTAATTATTTT	3119
Df	3354	TTATTAACTCTGAGCAGTATAGCATAATAAANCCCCGGGCAATTAATTATTTT	3413
QY	3120	CTTTTGTACATCTATTACAGTTTAGAAAAAACAAGCAATTTGTCAAAAAAATAAAAA	3179
Df	3414	CTTTTGTACATCTATTACAGTTTAGAAAAAACAAGCAATTTGTCAAAAAAATAAAAA	3473
QY	3180	AAAAAATAA 3188	
Df	3474	CTATTACAA 3482	
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US-10-159-563-308			
; Sequence 308, Application US/10159563			
; Publication No. US20040009154A1			
; GENERAL INFORMATION:			
; APPLICANT: Khan, Javed			
; APPLICANT: Ringner, Markus			
; APPLICANT: Peterson, Carsten			
; APPLICANT: Meltzer, Paul			
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR			
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS			
; FILE REFERENCE: 11613.56US11			
; CURRENT APPLICATION NUMBER: US/10/159,563			
; CURRENT FILING DATE: 2002-12-09			
; PRIOR APPLICATION NUMBER: US 10/133,937			
; PRIOR FILING DATE: 2002-04-25			
; NUMBER OF SEQ ID NOS: 444			
; SOFTWARE: Patent version 3.1			
; SEQ ID NO 308			
; LENGTH: 4459			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-159-563-308			
Query Match			
Best Local Similarity 96.8%; Score 3156.8; DB 17; Length 4459;			
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;			
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Df	294	ATGGGGAACGGGAGCGGGCTCCGGGCTCGGAGCTTTGGCCCGTACCCACGCTGCTG	353
QY	61	CTGCTCGCGCGGGCGCTACTGCGCGCTGTGCGAGCACTCGGGCGCCCTCCGAGGAGAC	120
Df	354	CTGCTCGCGCGGGCGCTACTGCGCGCTGTGCGAGCACTCGGGCGCCCTCCGAGGAGAC	413
QY	121	GAGGAGCTAGTGTGTCCGGAGCTGAGCGCGCCCGGAGACAGGGACCAACCGCCCTCCG	180
Df	414	GAGGAGCTAGTGTGTCCGGAGCTGAGCGCGCCCGGAGACAGGGACCAACCGCCCTCCG	473
QY	181	CTGCACGCGCTTTGACACAGCTGATCTGGAGCTGCGCGCCCGGAGACAGAGCTTTTGGCG	240
Df	474	CTGCACGCGCTTTGACACAGCTGATCTGGAGCTGCGCGCCCGGAGACAGAGCTTTTGGCG	533
QY	241	CCCGCTTTCAGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAA	300
Df	534	CCCGCTTTCAGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAA	593
QY	301	ACCGACTTGGGCGACTGTTCTATCCGGGACCGTGAATGGGATCCAGCTCGGCTGCC	360
Df	594	ACCGACTTGGGCGACTGTTCTATCCGGGACCGTGAATGGGATCCAGCTCGGCTGCC	653
QY	361	GCCCTCAGCCTTCGGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGTATTTC	420
Df	654	GCCCTCAGCCTTCGGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGTATTTC	713
QY	421	ATCCAGCGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCCCGCCAGGGGAGAGCGG	480
Df	714	ATCCAGCGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCCCGCCAGGGGAGAGCGG	773
QY	481	CGGGACCACTACAGTTTCCACTCTCTGCGGGGGAATCCGGAGGGGCGAGTATAGCGGCG	540
Df	774	CGGGACCACTACAGTTTCCACTCTCTGCGGGGGAATCCGGAGGGGCGAGTATAGCGGCG	833

QY	541	TGCGGGTCTGTGACGACGAGCCCGCGACTGGGAAAGCGAGACCGAAGACGAGGAC	600
DB	834	TGCGGGGTCTGTGACGACGAGCCCGCGACTGGGAAAGCGAGACCGAAGACGAGGAC	893
QY	601	GAAGGACCTGAGGGCGAGGACGAGGAGGCTCTAGTGTGCGCGAGACCGCGGACTGCAA	660
DB	894	GAAGGACCTGAGGGCGAGGACGAGGAGGCTCTAGTGTGCGCGAGACCGCGGACTGCAA	953
QY	661	GGCGTAGGACGAGCCACAGGACCTGAGGACGATGAAGGAGGAGGATTTGTGTCCAGTCA	720
DB	954	GGCGTAGGACGAGCCACAGGACCTGAGGACGATGAAGGAGGAGGATTTGTGTCCAGTCA	1013
QY	721	CGCTATGTGAAGACATCTTGTGGGACGACGATCGATGGGAGAAATTCACCGGAGTGT	780
DB	1014	CGCTATGTGAAGACATCTTGTGGGACGACGATCGATGGGAGAAATTCACCGGAGTGT	1073
QY	781	CTAAGCATTAACCTTCTCAGTTGTTTTCGGTGGGACGACGATGTGACAAACCCGAC	840
DB	1074	CTAAGCATTAACCTTCTCAGTTGTTTTCGGTGGGACGACGATGTGACAAACCCGAC	1133
QY	841	ATTCTGTAATTCAGTTAGCTTGTGCTGCTCCTCCTGCGGAACTTTTGGCAACTGGCAGAG	900
DB	1134	ATTCTGTAATTCAGTTAGCTTGTGCTGCTCCTCCTGCGGAACTTTTGGCAACTGGCAGAG	1193
QY	901	GGCGCGGAGTGAACCTTCAATGCTGCCCTCCTCCTGCGGAACTTTTGGCAACTGGCAGAG	960
DB	1194	GGCGCGGAGTGAACCTTCAATGCTGCCCTCCTCCTGCGGAACTTTTGGCAACTGGCAGAG	1253
QY	961	CAGCACACCCACCCAGTGAACCGGATGACGACCTATGACACAGCAATTTCTTTTCAAC	1020
DB	1254	CAGCACACCCACCCAGTGAACCGGATGACGACCTATGACACAGCAATTTCTTTTCAAC	1313
QY	1021	AGACAGACTTGTGTGGTCCAGACATGTGATCTCTTGGGATGCTGATGTGGAAC	1080
DB	1314	AGACAGACTTGTGTGGTCCAGACATGTGATCTCTTGGGATGCTGATGTGGAAC	1373
QY	1081	GTGTGTGATCCGAGCAGAGCTGCTCGTCTATGAGAGATGATGTTTACAGCTGCTTTC	1140
DB	1374	GTGTGTGATCCGAGCAGAGCTGCTCGTCTATGAGAGATGATGTTTACAGCTGCTTTC	1433
QY	1141	ACCACAGCCCATGAATTTAGGACCAAGCTGTTTAAATGACCATGATGATGACCAAGCTGT	1200
DB	1434	ACCACAGCCCATGAATTTAGGACCAAGCTGTTTAAATGACCATGATGATGACCAAGCTGT	1493
QY	1201	GCAGGCTTAAATGGTGTGAACGAGATTTCCACATGATGCTGCTTTCACAGCTG	1260
DB	1494	GCAGGCTTAAATGGTGTGAACGAGATTTCCACATGATGCTGCTTTCACACCTG	1553
QY	1261	GACACAGCCAGCTTGTGCTCTTGCAGTGCCTTACATGATTAATCATATTTCTGGATAAT	1320
DB	1554	GACACAGCCAGCTTGTGCTCTTGCAGTGCCTTACATGATTAATCATATTTCTGGATAAT	1613
QY	1321	GGTCATGGGAAATTTGTGAGGACCAAGCTCAGAAATCCCATACAGCTCCGAGGAGTCTC	1380
DB	1614	GGTCATGGGAAATTTGTGAGGACCAAGCTCAGAAATCCCATACAGCTCCGAGGAGTCTC	1673
QY	1381	CTGTGGACCTCGTACGATGCAACCGGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1440
DB	1674	CTGTGGACCTCGTACGATGCAACCGGAGTGCAGTTTACATTTGGGGAGGACTCCAAA	1733
QY	1441	CACCTGCTGATGACGAGCAGCATGTAGCAGCTTGTGTGATGACCGGACCTCTGTGGG	1500
DB	1734	CACCTGCTGATGACGAGCAGCATGTAGCAGCTTGTGTGATGACCGGACCTCTGTGGG	1793
QY	1501	GTGTGTGTGTCAAAACCAACACTTCCGCTGGGCGGATGGCAGCTGTGGAGAGGG	1560
DB	1794	GTGTGTGTGTCAAAACCAACACTTCCGCTGGGCGGATGGCAGCTGTGGAGAGGG	1853
QY	1561	AAATGGTGTATCAACCGGAGTGTGTGAACCAAAACCGACAGAAAGCATTTTGTATGACGCT	1620
DB	1854	AAATGGTGTATCAACCGGAGTGTGTGAACCAAAACCGACAGAAAGCATTTTGTATGACGCT	1913

QY	1621	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCGAGAACTGTCGGTGA	1680
DB	1914	TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCGAGAACTGTCGGTGA	1973
QY	1681	GGAGTCCAGTACACGATGAGGGAATGTGACAACTCCAGTCCCAAGAAATGAGGAGTAC	1740
DB	1974	GGAGTCCAGTACACGATGAGGGAATGTGACAACTCCAGTCCCAAGAAATGAGGAGTAC	2033
QY	1741	TGTGAAGGCAAACTGAGTGCCTTACAGATCCTGTAACTTTGAGGACTGTCCAGCAATAAT	1800
DB	2034	TGTGAAGGCAAACTGAGTGCCTTACAGATCCTGTAACTTTGAGGACTGTCCAGCAATAAT	2093
QY	1801	GGAAAACTTTTGTAGAGAGGAACAATGTGAAGCACAACAAGTGTTCAAAAGTCTCTTT	1860
DB	2094	GGAAAACTTTTGTAGAGAGGAACAATGTGAAGCACAACAAGTGTTCAAAAGTCTCTTT	2153
QY	1861	GGAGTGGGCTTGGGATGGATTCCTCAAGTACGCTGGGCTCTCACCAAGGACAGG	1920
DB	2154	GGAGTGGGCTTGGGATGGATTCCTCAAGTACGCTGGGCTCTCACCAAGGACAGG	2213
QY	1921	TGCAAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTGGTTTGTGAGCCCAAGGTT	1980
DB	2214	TGCAAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTGGTTTGTGAGCCCAAGGTT	2273
QY	1981	GTAGATGGTACTCCATGTAGCCAGATTCCTCTGTCTGTGTGCAAGGACAGTGTGA	2040
DB	2274	GTAGATGGTACTCCATGTAGCCAGATTCCTCTGTCTGTGTGCAAGGACAGTGTGA	2333
QY	2041	AAAGCTGGTGTGATCGCATCATGACTCCAAAAGAACTTTGATAAATGTGTGTTC	2100
DB	2334	AAAGCTGGTGTGATCGCATCATGACTCCAAAAGAACTTTGATAAATGTGTGTTC	2393
QY	2101	GGGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA	2160
DB	2394	GGGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA	2453
QY	2161	TATCATGATATCATCAAAATTCAGTGGAGCCACCAATCGAAGTGAACAGCGGAAC	2220
DB	2454	TATCATGATATCATCAAAATTCAGTGGAGCCACCAATCGAAGTGAACAGCGGAAC	2513
QY	2221	CAGAGGGATCCAGGAACTATGGCAGCTTCTTGGCCATCAAGCTGCTGATGCAATAT	2280
DB	2514	CAGAGGGATCCAGGAACTATGGCAGCTTCTTGGCCATCAAGCTGCTGATGCAATAT	2573
QY	2281	ATTCTTAAATGGTGTACTACTTGTCCACTTAGAGCAAGACATTAATGTACAAAGTGT	2340
DB	2574	ATTCTTAAATGGTGTACTACTTGTCCACTTAGAGCAAGACATTAATGTACAAAGTGT	2633
QY	2341	GTCTTGAGGTACAGCGGCTCTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC	2400
DB	2634	GTCTTGAGGTACAGCGGCTCTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC	2693
QY	2401	AAAGAGCTTGTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATATAA	2460
DB	2694	AAAGAGCTTGTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATATAA	2753
QY	2461	TACACCTTACTTCTTAAAGAGAAAGAAAGTCTTCAATGCTATCCCACTTTTTCAGCA	2520
DB	2754	TACACCTTACTTCTTAAAGAGAAAGAAAGTCTTCAATGCTATCCCACTTTTTCAGCA	2813
QY	2521	TGGGTCAATTAAGAGTGGGCGGAATGTCTAAGTCAATGTGAATGGGTGGCAGAGAGA	2580
DB	2814	TGGGTCAATTAAGAGTGGGCGGAATGTCTAAGTCAATGTGAATGGGTGGCAGAGAGA	2873
QY	2581	CTGGTAGAATGCCGAGACATTAATGACAGCTGCTTCCGAGTGTCCAAAGGAGTGAAG	2640
DB	2874	CTGGTAGAATGCCGAGACATTAATGACAGCTGCTTCCGAGTGTCCAAAGGAGTGAAG	2933
QY	2641	CCAGCCAGCAGACAGACTTGTGAGACCACTCCCTGCCCCCAGTGGGAGTGG	2700
DB	2934	CCAGCCAGCAGCAGACTTGTGAGACCACTCCCTGCCCCCAGTGGGAGTGG	2993
QY	2701	TCATCATGTTTCTAAGACCTGTGGGAGGGTTACAAAAAAGAAAGCTTTGAAGTGTCTCTCC	2760


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Qy 2821 ATAGACTTTTGCACAAATGCGAAGTGCAGTTAAGTGGTTTAAAGTGGTTAGCTTTGA-G 2879
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Db 3414 CTTTGTGTACATCTATTACAGTTTAGAAAAAACAAGCAATGTCAAAAAAAGTAGAA 3473
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RESULT 14

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US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17
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Query Match 96.8%; Score 3156.8; DB 10; Length 4760;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
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Db 612 ATGGGGAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCGTACCCACGCTGCTG 671
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Db 792 CTGACGCGCTTTGACCAAGCACTGGATCTGAGCTGCGGCGCCGACAGCAGCTTTTGGCG 851
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Db 852 CCGCGCTTCAAGCTCCAGAAAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGGAA 911
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; APPLICANT: Rubin, Mark A.									
; APPLICANT: Sreekumar, Arun									
; TITLE OF INVENTION: Expression Profile of Prostate Cancer									
; FILE REFERENCE: UM-07221									
; CURRENT APPLICATION NUMBER: US/10/210,120									
; CURRENT FILING DATE: 2002-08-01									
; PRIOR APPLICATION NUMBER: US 60/309,581									
; PRIOR FILING DATE: 2001-08-02									
; PRIOR APPLICATION NUMBER: US 60/334,468									
; PRIOR FILING DATE: 2001-11-15									
; NUMBER OF SEQ ID NOS: 123									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 57									
; LENGTH: 4309									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
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Best Local Similarity 99.5%; Pred No. 0;									
Matches 3174; Conservative 0; Mismatches 14; Indels 1; Gaps 1;									
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QY	61	CTGCTCGCGCGGCGCTACTGCGCTGTGCGAGCACTCGGGGCGCCCTCCGAGGAGAC	120						
DB	227	CTGCTCGCGCGGCGCTACTGCGCTGTGCGAGCACTCGGGCGCCCTCCGAGGAGAC	286						
QY	121	GAGGAGCTAGTGTGCGCGAGCTGCGAGCGCGCCCGGGACACGGACACCGCGCTCCGC	180						
DB	287	GAGGAGCTAGTGTGCGCGAGCTGCGAGCGCGCCCGGGACACCGAGCAACCGCGCTCCGC	346						
QY	181	CTGCACGCTTTGACGAGCAGCTGATCTGGAGCTGCGGCGCGACAGCAGCTTTTGGCG	240						
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QY	241	CCGCGCTTACGCTCCAGAACGTGGGGCGCAATCGGGTCGAGACGCGCTTCCGGA	300						
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QY	301	ACCGACTTGGCGCACTGCTTCTACTCCGCACTGGTGAATGGCGATCCAGCTCGGCTGCC	360						
DB	467	ACCGACTTGGCGCACTGCTTCTACTCCGCACTGGTGAATGGCGATCCAGCTCGGCTGCC	526						
QY	361	GCCCTCAGCTCTGCGAGGCGTGGCGGCGCTTCTACTGCTGGGAGGCGTATTTC	420						
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QY	541	TGCGGGGTGTTGGAAGAGCGAGCGCGCGGAGTGGGAAAGCGGAGACGAGAGAG	600						
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QY	601	GAAGGAGCTGAGGGCGAGGAGCAAGGGCTCAGTGTGCGCGCAGAGCCCGGCACTGCA	660						
DB	767	GAAGGAGCTGAGGGCGAGGAGCAAGGGCTCAGTGTGCGCGCAGAGCCCGGCACTGCA	826						
QY	661	GGCGTAGGACACCCACAGGAATCGGAGCATAGAAAGAGCGATTTGTGTCAGTCCAC	720						
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QY	721	CGCTATGTGGAACCAATGCTTGTGGCAGACCAAGTGCATGGGAGGAATTCACGCGAGTGT	780						
DB	887	CGCTATGTGGAACCAATGCTTGTGGCAGACCAAGTGCATGGGAGGAATTCACGCGAGTGT	946						

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QY	841	ATTCGTAATTCAGTTAGCTGCTGCTGCTGAAGATCTTGGTCATCCAGATGAAACAGAG	900
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QY	961	CAGCACACCCACCCAGTGACCGGGATCGAGGCACTATGACACAGCAATCTTTTTCACC	1020
DB	1127	CAGCACACCCACCCAGTGACCGGGATCGAGGCACTATGACACAGCAATCTTTTTCACC	1186
QY	1021	AGACAGGACTTGTGTGGGTCCACAGCATGTGATCTCTTGGGATGGCTGATTTGGAACT	1080
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QY	1081	GTGTGTATCCGAGCAGAAAGCTGCTCCGTCTATAGAAGATGATGGTTTCAAGCTGCTTC	1140
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QY	1141	ACCACAGCCCATGAATTAAGGCCACGTGTTTAAACATGCCACATGATGATGCAAGCAGTGT	1200
DB	1307	ACCACAGCCCATGAATTAAGGCCACGTGTTTAAACATGCCACATGATGATGCAAGCAGTGT	1366
QY	1201	GCCAGCCTTAATGTGTGAACCCAGGATTTCCACATGATGGGCTCAATGCTTTCCAACTG	1260
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9996.978 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2904	72.3	4858	3	US-09-392-184-1
3	2471	61.6	3889	4	US-09-568-559-1
4	2090	52.1	3706	3	US-09-494-970B-58
5	1303	32.5	2184	4	US-09-445-023A-2
6	67	1.7	260	4	US-09-513-999C-32662
7	38	0.9	2184	4	US-09-445-023A-13
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9	29	0.7	1211	3	US-09-063-743-2
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26	26	0.6	8519	3	US-09-261-907-1
27	25	0.6	266	4	US-09-023-655-693

ALIGNMENTS

RESULT 1

US-09-130-491-1
; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-09-130-491-1

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QY 325 GCTCTGCGCGCCTTCCACAGTAATAGAAATGTTAAATTTTAAACAATCCACAGACGCG 384
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RESULT 3
 US-09-568-559-1
 ; Sequence 1, Application US/09568559
 ; Patent No. 6649377
 ; GENERAL INFORMATION:
 ; APPLICANT: Klonowski, Paul
 ; APPLICANT: Allard, John
 ; APPLICANT: Heller, Renu
 ; APPLICANT: Van Wart, Harold
 ; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
 ; TITLE OF INVENTION: Compositions Encoding the Same
 ; FILE REFERENCE: ROCH-002
 ; CURRENT APPLICATION NUMBER: US/09/568,559
 ; CURRENT FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: 60/133,343
 ; PRIOR FILING DATE: 1999-05-10
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3889
 ; TYPE: DNA
 ; ORGANISM: human
 ; US-09-568-559-1

Query Match 61.6%; Score 2471; DB 4; Length 3889;
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 Matches 3221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 2096 AGTGTGTGAACAAACACACAGAAAGCAATTTTGATACCGCTTTTCATGGAAGCTGGGAA 2155
Db 1638 AGTGTGTGAACAAACACACAGAAAGCAATTTTGATACCGCTTTTCATGGAAGCTGGGAA 1697
Qy 2156 TGTGGGGGCTTTGGGAGAGCTGTTCCAGAACTGTCGGTGGAGAGTCCAGTATACAGATCA 2215
Db 1698 TGTGGGGGCTTTGGGAGAGCTGTTCCAGAACTGTCGGTGGAGAGTCCAGTATACAGATCA 1757
Qy 2216 GGGAAATGTGAACAAACCCAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGGCAACAGATGC 2275
Db 1758 GGGAAATGTGAACAAACCCAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGGCAACAGATGC 1817
Qy 2276 GCTACAGATCTCTGTAACTTGGAGAGCTGTCAGACAAATAATGGAAGAACTTTAGAGAG 2335
Db 1818 GCTACAGATCTCTGTAACTTGGAGAGCTGTCAGACAAATAATGGAAGAACTTTAGAGAG 1877
Qy 2336 AACAAATGTGAAGCACAACAGATTTTCAAAAGCTTCTTTGGGAGTGGGCTGCGGTGG 2395
Db 1878 AACAAATGTGAAGCACAACAGATTTTCAAAAGCTTCTTTGGGAGTGGGCTGCGGTGG 1937
Qy 2396 AATGGAATTTCCAAAGTACGCTGGCGTCTCACAAAGGACAGAGTGCAGCTCATCTGCCAAG 2455
Db 1938 AATGGAATTTCCAAAGTACGCTGGCGTCTCACAAAGGACAGAGTGCAGCTCATCTGCCAAG 1997
Qy 2456 CCAAAAGGCAATTTGGCTACTCTTCTGTTTGCAGCCCAAGTGTAGATGGTACTCATGTA 2515
Db 1998 CCAAAAGGCAATTTGGCTACTCTTCTGTTTGCAGCCCAAGTGTAGATGGTACTCATGTA 2057
Qy 2516 GCCAGATTTCCACCTCTGCTGTGTGCAAGGACAGTGTGTAAGCTGTTGTGATCGCA 2575
Db 2058 GCCAGATTTCCACCTCTGCTGTGTGCAAGGACAGTGTGTAAGCTGTTGTGATCGCA 2117
Qy 2576 TCATAGACTCCAAAGAAAGTGTGATAAATGTTGGTGTTCGCGGGGAAATGGATCTACTT 2635
Db 2118 TCATAGACTCCAAAGAAAGTGTGATAAATGTTGGTGTTCGCGGGGAAATGGATCTACTT 2177
Qy 2636 GTAAAAAATATCAGGATCAGTTACTAGTGCAGAACTGGATATCATGATATCATCAAA 2695
Db 2178 GTAAAAAATATCAGGATCAGTTACTAGTGCAGAACTGGATATCATGATATCATCAAA 2237
Qy 2696 TTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGAACCAGAGGGGATCCAGGAACA 2755
Db 2238 TTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGAACCAGAGGGGATCCAGGAACA 2297
Qy 2756 ATGGCAGCTTTCTTGCATCAAAAGCTGCTGATGGCACATATATTCTTAATGGTACTACA 2815
Db 2298 ATGGCAGCTTTCTTGCATCAAAAGCTGCTGATGGCACATATATTCTTAATGGTACTACA 2357
Qy 2816 CTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTTGCTTTGAGGTACAGGGCT 2875
Db 2358 CTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTTGCTTTGAGGTACAGGGCT 2417
Qy 2876 CTTTGTGGGCAATGCGCCTTTAGCCCTTTCAGAGGCTTCAAAAGGCTTTGACCATCC 2935
Db 2418 CTTTGTGGGCAATGCGCCTTTAGCCCTTTCAGAGGCTTCAAAAGGCTTTGACCATCC 2477
Qy 2936 AGGTTCTTACTGTGGGCAATGCGCCTTTGCACTTAAATTAATACTTCTTCTGTAAGA 2995
Db 2478 AGGTTCTTACTGTGGGCAATGCGCCTTTGCACTTAAATTAATACTTCTTCTGTAAGA 2537
Qy 2996 AGAAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAGAGTGGG 3055
Db 2538 AGAAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAGAGTGGG 2597
Qy 3056 GCGAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAGACTGGTAGAATGCCAGACA 3115
Db 2598 GCGAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAGACTGGTAGAATGCCAGACA 2657
Qy 3116 TTAAATGGAAGCGCTTCTCGAGTGTGCAAGAGGAAATGGAAGCGAGCAGCACTTCTT 3175

Db 2658 TTAATGACAGCGCTGCTCCGAGTGTGCAAAAGGAGTGAAAGCCAGCCAGCAACAGACCTT 2717
Qy 3176 GTGACAGACCATCCCTGCCCCCAGTGTGACGTGGGGAGTGGTCAATCATCTTCTAAGACCT 3235
Db 2718 GTGACAGACCATCCCTGCCCCCAGTGTGACGTGGGGAGTGGTCAATCATCTTCTAAGACCT 2777
Qy 3236 GTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGAGGGGTGTTAT 3295
Db 2778 GTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGAGGGGTGTTAT 2837
Qy 3296 CTCATGACAGCTGTGATCTCTTAAAGAACCTTAAACATTTTATAGACTTTTGCACAAATGG 3355
Db 2838 CTCATGACAGCTGTGATCTCTTAAAGAACCTTAAACATTTTATAGACTTTTGCACAAATGG 2897
Qy 3356 CAGAAATGCAAGTTAAGTGGTTAAGTGGTTAGCTTTGAGGGCAAGCAAGAGTGAAGAAAG 3415
Db 2898 CAGAAATGCAAGTTAAGTGGTTAAGTGGTTAGCTTTGAGGGCAAGCAAGAGTGAAGAAAG 2957
Qy 3416 GGCTGGTCAGGGAAGAGCAAGAGGCTGGAGGGATCCAGGTATCTTCCAGTAACCACT 3475
Db 2958 GGCTGGTCAGGGAAGAGCAAGAGGCTGGAGGGATCCAGGTATCTTCCAGTAACCACT 3017
Qy 3476 GAGGTGTATCAGTAAGCTGGATTATGGGGTAGATAGAAAGGAGTTGAATCATCAGAG 3535
Db 3018 GAGGTGTATCAGTAAGCTGGATTATGGGGTAGATAGAAAGGAGTTGAATCATCAGAG 3077
Qy 3536 TAAACTGCCAGTTGCAAAATTTGATAGATAGTTAGTGAAGTATTAACTCTGAGCAGT 3595
Db 3078 TAAACTGCCAGTTGCAAAATTTGATAGATAGTTAGTGAAGTATTAACTCTGAGCAGT 3137
Qy 3596 GATATAGCATATAAAGCCCGGGCATTATTAATTAATTTCTTTTGTGTACATCTACTAC 3655
Db 3138 GATATAGCATATAAAGCCCGGGCATTATTAATTAATTTCTTTTGTGTACATCTACTAC 3197
Qy 3656 AGTTTAGAAAAAACAAGCAATGTCAAAAAAGTTAGAACTATTACAAACCCCTG 3711
Db 3198 AAGTTTAGAAAAAACAAGCAATGTCAAAAAAGTTAGAACTATTACAAACCCCTG 3253

RESULT 4

US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 007074.1
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Query Match 52.1%; Score 2090; DB 3; Length 3706;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2610; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Qy 1034 GGCAGGGCGAGTGGCGGACAGTGGGGGTCTGTGACGACGAGCCCCCGCCGACTGGGA 1093
Db 1 GGCAGGGCGAGTGGCGGACAGTGGGGGTCTGTGACGACGAGCCCCCGCCGACTGGGA 60

Qy 1094 AAGCGGAGACCGAAGACGAGGACGAAAGGAGCTGAGGGCGAGGACGAGGGCCTCAGTGGT 1153
Db 61 AAGCGGAGACCGAAGACGAGGACGAAAGGAGCTGAGGGCGAGGACGAAAGGGCCTCAGTGGT 120
Qy 1154 CCGCGCAGGACCGGACCTGCAAGCGGTAGGACAGCCACAGGAACTGCAAGCATAAAGAA 1213
Db 121 CCGCGCAGGACCGGACCTGCAAGCGGTAGGACAGCCACAGGAACTGCAAGCATAAAGAA 180
Qy 1214 AGAAGCGATTTGTCTCAGTCAACCGTATGTGGAAACCAATGTCTTGGGAGACCACTCGA 1273
Db 181 AGAAGCGATTTGTCTCAGTCAACCGTATGTGGAAACCAATGTCTTGGGAGACCACTCGA 240
Qy 1274 TGGCAGAAATTCACGGCAGTGTCTAAAGCATTTCTCTCAGTGTCTTGGTGGCAG 1333
Db 241 TGGCAGAAATTCACGGCAGTGTCTAAAGCATTTCTCTCAGTGTCTTGGTGGCAG 300
Qy 1334 CCAGATTTGACAAACACCCACAGCATTTCTGTAATTCAGTTAGCTTGGTGGTGAAGATCT 1393
Db 301 CCAGATTTGACAAACACCCACAGCATTTCTGTAATTCAGTTAGCTTGGTGGTGAAGATCT 360
Qy 1394 TGGTCATCCAGATGAACAGAGGGGCCGAAAGTGAACCTTCAATGTCTGCCCTCAGTCTGC 1453
Db 361 TGGTCATCCAGATGAACAGAGGGGCCGAAAGTGAACCTTCAATGTCTGCCCTCAGTCTGC 420
Qy 1454 GGAATTTTGGCACTGGCAGAGAGCAGCAACCCACCCAGTGAACCGGATGACAGCACT 1513
Db 421 GGAATTTTGGCACTGGCAGAGAGCAGCAACCCACCCAGTGAACCGGATGACAGCACT 480
Qy 1514 ATGACACAGCAATTTCTTTTACCAGACAGGACTTTGTGGTGGTCCAGACATGTGATACTC 1573
Db 481 ATGACACAGCAATTTCTTTTACCAGACAGGACTTTGTGGTGGTCCAGACATGTGATACTC 540
Qy 1574 TTGGGATGGCTGATTTTGGAACTGTGTGATCCGAGCAGAAAGCTCTCCGTCAATGAAG 1633
Db 541 TTGGGATGGCTGATTTTGGAACTGTGTGATCCGAGCAGAAAGCTCTCCGTCAATGAAG 600
Qy 1634 ATGATGGTTTACAGCTGCTTCCACACAGCCCATGAATAGGCCAGCTGTTTAAATGC 1693
Db 601 ATGATGGTTTACAGCTGCTTCCACACAGCCCATGAATAGGCCAGCTGTTTAAATGC 660
Qy 1694 CACATGATGATCAAAAGCAGTGTGCCAGCTTAAATGTGTGAACACAGGATTTCCACATGA 1753
Db 661 CACATGATGATCAAAAGCAGTGTGCCAGCTTAAATGTGTGAACACAGGATTTCCACATGA 720
Qy 1754 TGGCGTCAATGTCTTCCAACTGGACACAGCCAGCTTGGTCTCTCTTGCAGTGGCTACA 1813
Db 721 TGGCGTCAATGTCTTCCAACTGGACACAGCCAGCTTGGTCTCTCTTGCAGTGGCTACA 780
Qy 1814 TGATTAATCATCTTCTGGATTAATGTGTGATGGGAAATTTGTGAGCAAGCCTCAGNATC 1873
Db 781 TGATTAATCATCTTCTGGATTAATGTGTGATGGGAAATTTGTGAGCAAGCCTCAGNATC 840
Qy 1874 CCATACAGTCCCAGGCGATCTCCCTGGCACCTCGTACGATGCCAACCCGAGTGGCCAGT 1933
Db 841 CCATACAGTCCCAGGCGATCTCCCTGGCACCTCGTACGATGCCAACCCGAGTGGCCAGT 900
Qy 1934 TTACATTTGGGAGGAGCTCCAAACACTGCCCTGATGCAGCCAGCAGCATGTAGCACTTGT 1993
Db 901 TTACATTTGGGAGGAGCTCCAAACACTGCCCTGATGCAGCCAGCAGCATGTAGCACTTGT 960
Qy 1994 GGTGTACCGGACCTCTGTGGGGTGTGTGTGATCAACCAACCACTTCCGTGGGGCGG 2053
Db 961 GGTGTACCGGACCTCTGTGGGGTGTGTGTGATCAACCAACCACTTCCGTGGGGCGG 1020
Qy 2054 ATGGCACAGCTGTGAGAGGGAATGGTATCAACGGCAAGTGTGCAACAAACACC 2113
Db 1021 ATGGCACAGCTGTGAGAGGGAATGGTATCAACGGCAAGTGTGCAACAAACACC 1080
Qy 2114 ACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAAATGTGGGGCCTTGGGGAG 2173
Db 1081 ACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAAATGTGGGGCCTTGGGGAG 1140
Qy 2174 ACTGTTGAGAAAGTGGGGTGGAGGAGTCCAGTACAGATGAGGGGAATGTGACAAACCCAG 2233

|||||
Db 1141 ACTGTTGAGAACGTCGCGTGAGGAGTCCAGTACACGATGAGGGATGTGACACCCG 1200
QY 2234 TCCCAAGAAATGAGGGAAGTACTGTGAAGCAACAGATGCGCTACAGATCCTGTAAAC 2293
Db 1201 TCCCAAGAAATGAGGGAAGTACTGTGAAGCAACAGATGCGCTACAGATCCTGTAAAC 1260
QY 2294 TTGAGGACTGTCCAGACAAATATGNAACCTTTAGAGAGGAACAAATGTGAAGCACACA 2353
Db 1261 TTGAGGACTGTCCAGACAAATATGNAACCTTTAGAGAGGAACAAATGTGAAGCACACA 1320
QY 2354 ACAGATTTTCAAAAGCTCTCTTTGGGAGTGCGCTGCGGTGGAATGGATTTCCCAAGTAGC 2413
Db 1321 ACAGATTTTCAAAAGCTCTCTTTGGGAGTGCGCTGCGGTGGAATGGATTTCCCAAGTAGC 1380
QY 2414 CTGGCGTCTCAACAAAGGACAGGTGCAAGCTCATCTGCCAACCCAAAGGCAATGGCTACT 2473
Db 1381 CTGGCGTCTCAACAAAGGACAGGTGCAAGCTCATCTGCCAACCCAAAGGCAATGGCTACT 1440
QY 2474 TCTTCGTTTTCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATTTCCACTCTG 2533
Db 1441 TCTTCGTTTTCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATTTCCACTCTG 1500
QY 2534 TCTGTGTGCAAGGACAGGTGTAAAAGCTGGTGTGATCGCATCATAGACTCCAAAAGA 2593
Db 1501 TCTGTGTGCAAGGACAGGTGTAAAAGCTGGTGTGATCGCATCATAGACTCCAAAAGA 1560
QY 2594 AGTTTGATATAATGTGGTGTTCGGGGGAAATGGATCTACTTGTAAAAAATATCAGAT 2653
Db 1561 AGTTTGATATAATGTGGTGTTCGGGGGAAATGGATCTACTTGTAAAAAATATCAGAT 1620
QY 2654 CAGTTACTAGTGCAAAACCTCGATATCATGATATCATCAATTCCACTGAGCCACCA 2713
Db 1621 CAGTTACTAGTGCAAAACCTCGATATCATGATATCATCAATTCCACTGAGCCACCA 1680
QY 2714 ACATCGAAGTGAACACAGCGGAACACAGAGGGGATCAGGAACAAT-GGCAGCTTTCTTGCC 2772
Db 1681 ACATCGAAGTGAACACAGCGGAACACAGAGGGGATCAGGAACAATGGCAGCTTTCTTGCC 1740
QY 2773 ATCAAAGCTGTGATGGACATATATCTTAATGTGACTACACTTTGTCACCTTAGAG 2832
Db 1741 ATCAAAGCTGTGATGGACATATATCTTAATGTGACTACACTTTGTCACCTTAGAG 1800
QY 2833 CAAGCATTATGTACAAAGGTGTCTGTAGGTACAGCGGTCTCTGCGGCATTTGNA 2892
Db 1801 CAAGCATTATGTACAAAGGTGTCTGTAGGTACAGCGGTCTCTGCGGCATTTGNA 1860
QY 2893 AGAATTCGAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGC 2952
Db 1861 AGAATTCGAGCTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGC 1920
QY 2953 AATGCCCTTCGACCTAAATTAATATACACTTCTGTAAGAGAGAGGAAGAAATCTTTTC 3012
Db 1921 AATGCCCTTCGACCTAAATTAATATACACTTCTGTAAGAGAGAGGAAGAAATCTTTTC 1980
QY 3013 ATGTCTATCCCACTTTTTCAGATGGGTCAATGAGAGTGGGGCAATGTCTAAGTCA 3072
Db 1981 AATGTCTATCCCACTTTTTCAGATGGGTCAATGAGAGTGGGGCAATGTCTAAGTCA 2040
QY 3073 TGTGAATTTGGGTGGCAGAGAGACTGGTGAATGCCAGACATTAATGGAAGAGGCTGTCT 3132
Db 2041 TGTGAATTTGGGTGGCAGAGAGACTGGTGAATGCCAGACATTAATGGAAGAGGCTGTCT 2100
QY 3133 TCCGAGTGTGCAAGGAAGTGAAGCCAGCAGACCAAGACCTTTGTGAGACCAATCCCTGCG 3192
Db 2101 TCCGAGTGTGCAAGGAAGTGAAGCCAGCAGACCAAGACCTTTGTGAGACCAATCCCTGCG 2160
QY 3193 CCCAGTGTGCAAGTGGGAGGTGATCATCTTCTTAAGACCTGTGGGAGGTTTACAAA 3252
Db 2161 CCCAGTGTGCAAGTGGGAGGTGATCATCTTCTTAAGACCTGTGGGAGGTTTACAAA 2220
QY 3253 AAAACAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTATCTCATGACAGCTGTGAT 3312
|||||

Db 2221 AAAAGAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTCTTATCTCATGAGAGCTGTGAT 2280
QY 3313 CTTTTAAAGAAACCTTAAACATTTTATAGACTTTTGCACAAATGGCGAAGATGCAAGTTAAGTG 3372
Db 2281 CTTTTAAAGAAACCTTAAACATTTTATAGACTTTTGCACAAATGGCGAAGATGCAAGTTAAGTG 2340
QY 3373 GTTTAAGTGGTGTAGCTTTGAGGGCAGGCAAGCTGAGGAGGGCTGGTGCAGGGAAG 3432
Db 2341 GTTTAAGTGGTGTAGCTTTGAGGGCAGGCAAGCTGAGGAGGGCTGGTGCAGGGAAG 2400
QY 3433 CAAGAAGGCTGAGGAGGATCCAGCGTATCTTCCAGTAAACCACTGAGGTGTATCAGTAAGG 3492
Db 2401 CAAGAAGGCTGAGGAGGATCCAGCGTATCTTCCAGTAAACCACTGAGGTGTATCAGTAAGG 2460
QY 3493 TGGGATTAATGGGGGTAGATAGAAAAGAGTGAATCATCATCAGAGTAAACTGCCAGTTGCAA 3552
Db 2461 TGGGATTAATGGGGGTAGATAGAAAAGAGTGAATCATCATCAGAGTAAACTGCCAGTTGCAA 2520
QY 3553 ATTTGATAGGATAGTGTAGTGGATTTAATCCTCTGAGCAGTGTATATAGCATATAATAAG 3612
Db 2521 ATTTGATAGGATAGTGTAGTGGATTTAATCCTCTGAGCAGTGTATATAGCATATAATAAG 2580
QY 3613 CCCCAGGCAATTAATTAATTAATTTCTTTTGTATCATCTA 3651
Db 2581 CCCCAGGCAATTAATTAATTAATTTCTTTTGTATCATCTA 2619

RESULT 5

US-09-445-023A-2

; Sequence 2, Application US/09445023A

; Patent No. 6565858

; GENERAL INFORMATION:

; APPLICANT: Hirose, Kunitaka

; APPLICANT: Inoguchi, Eiichi

; APPLICANT: Hakozaaki, Michinori

; APPLICANT: Ishioka, Keiko

; APPLICANT: Ishida, Yukako

; APPLICANT: Matsushima, Kouji

; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS-

; FILE REFERENCE: Q57092

; CURRENT APPLICATION NUMBER: US/09/445,023A

; CURRENT FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: JP 9-160422

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 2184

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: exon

; LOCATION: (1) .. (2184)

US-09-445-023A-2

Query Match 32.5%; Score 1303; DB 4; Length 2184;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 2003; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1240 TATGTGGAACCATCTTGTGGCAGACCACTCGATGGCAGAAATCCACGGCAGTGTCTTA 1299

Db 55 TATGTGGAACCATCTTGTGGCAGACCACTCGATGGCAGAAATTCACGGCAGTGTCTTA 114

QY 1300 AAGCAATTACCTTCTCAACGTTGTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGCATTT 1359

Db 115 AAGCAATTACCTTCTCAACGTTGTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGCATTT 174

QY 1360 CGTAATTCAGTTAGTCTGGTGGTGAAGATCTTTGGTTCATCCAGATGAACAGAGGGG 1419

Db 175 CGTAATTCAGTTAGTCTGGTGGTGAAGATCTTTGGTTCATCCAGATGAACAGAGGGG 234

1420 CCAGAGTACCTCAATGCTGCTCCTCACTGCGGAACTTTTGCACTGGCAGAGCAG 1479
1480 CACAAACCCACCAAGTACCGGGATGAGAGCACTATGACACAGCAATCTTTTACCAGA 1539
1540 CAGGACTGTGGTGGTCCAGACATGATGATGATGATGATGATGATGATGATGATGATG 1599
1600 TGTGATCCAGCAGAGAGTGTCTCCGTCATAGAGATGATGATGATGATGATGATGATG 1659
1660 ACAGCCCATGAATTAGGCCACGTTGTTTAAATGCCACATGATGATGATGATGATGATG 1719
1720 AGCCTTAATGGTGTGAACCAAGGATCCCAATGATGATGATGATGATGATGATGATGAT 1779
1780 CACAGCCAGCTTGGTCTCCTGTCAGTGGCTACATGATGATGATGATGATGATGATGAT 1839
1840 CATGGGGAATTTGTGATGGAACAAGCCCTCAGAATCCCATAGCTCCAGGCGATCCCT 1899
1900 GGCACCTGTGACATGACCAACCGGAGTCCAGTTTACATTTTGGGAGGAGTCCCAACAC 1959
1960 TGCCCTGTATGACGACGACATGTAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2019
2020 CTGGTGTGTCACAAACCAACTTTCCGCTGGCGGATGGCACCACTGCTGAGAGGAA 2079
2080 TGGTGTATCAACGCGAGTGTGGAACAAACCAAGCAATTTTGTATGACCTTTT 2139
2140 CATGGAAGCTGGGGAATGTGGGGCTTGGGGAGCTGTTTGGAGAACGCTGGGTGGAGGA 2199
2200 GTCCAGTACACGATGAGGGAATGTGACACCCAGTCCCAAGAAATGAGGGAATGACTGT 2259
2260 GAGGCAAAACGATGCGCTACAGATCTCTGTAACTTGGAGCTCTCCAGCAATATGGA 2319
2320 AARACCTTTAGAGAGGAACATGTGAAGACACAAACAGTCTTCAAAAGCTCTCTTTGGG 2379
2380 AGTGGGCTGCGGTGGAATGGAATCCCAAGTACGCTGGCGTCTCACCAAGGACAGTGC 2439
2440 AAGTCTATCTGCCAAGCAAGGATTTGGCTTCTCTGTTTGGAGCCCAAGGTTGTA 2499
2500 GATGGTACTCAATGATGCCAGATTTCCACCTCTCTGCTGTGTCAGGACAGTGTGTA 2559

1315 GATGGTACTCCATGTAGCCAGATTCACCTCTGCTGTGTGTCAGGACAGTGTGTAA 1374
2560 GCTGGTGTGATCGCATCATAGACTCCAAAAGAGAGTTTGTATAAATGTGTGTTCGGG 2619
1375 GCTGGTGTGATCGCATCATAGACTCCAAAAGAGAGTTTGTATAAATGTGTGTTCGGG 1434
2620 GGAATGGAATCTACTTTGTAAAAAATATCAGGATCAGTTTACTAGTGCAAAACCTGGAT 2679
1435 GGAATGGAATCTACTTTGTAAAAAATATCAGGATCAGTTTACTAGTGCAAAACCTGGAT 1494
2680 CATGATATCATCAATTTCAAACCTGGAGCCCAACATCGAAGTGAACAGCGGACAG 2739
1495 CATGATATCATCAATTTCAAACCTGGAGCCCAACATCGAAGTGAACAGCGGACAG 1554
2740 AGGGGATCCAGGAACAATGCGAGCTTTCTTGCCATCAAAAGCTGCTGATGGCAATAT 2799
1555 AGGGGATCCAGGAACAATGCGAGCTTTCTTGCCATCAAAAGCTGCTGATGGCAATAT 1614
2800 CTTAATGCTGACTACACTTTTGTCCACTTTAGAGCAAGACATTATGTACAAAGTGTGTC 2859
1615 CTTAATGCTGACTACACTTTTGTCCACTTTAGAGCAAGACATTATGTACAAAGTGTGTC 1674
2860 TTGAGGTA CAGCGGCTCTCTGCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTCAA 2919
1675 TTGAGGTA CAGCGGCTCTCTGCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTCAA 1734
2920 GAGCCCTTCCACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACTTAAATTAATAC 2979
1735 GAGCCCTTCCACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACTTAAATTAATAC 1794
2980 ACCTACTTCTGTAAGAGAGAGGAAATCTTCAATGCTATCCCACTTTTTCAGCATGG 3039
1795 ACCTACTTCTGTAAGAGAGAGGAAATCTTCAATGCTATCCCACTTTTTCAGCATGG 1854
3040 GTCAITTAAGAGAGTGGGCGCAATGTTCTAAGTCAATGTGAATGGTGGCGAGAGACTG 3099
1855 GTCAITTAAGAGAGTGGGCGCAATGTTCTAAGTCAATGTGAATGGTGGCGAGAGACTG 1914
3100 GTAGAATGCGGAGACATTAATGACAGCTGTTTCCGAGTGTGCAAGAGAGTGAAGCCA 3159
1915 GTAGAATGCGGAGACATTAATGACAGCTGTTTCCGAGTGTGCAAGAGAGTGAAGCCA 1974
3160 GCAGACACAGACCTTTGTGTCAGACCATCTCTGCCCCCAGTGGGAGTGGTCA 3219
1975 GCAGACACAGACCTTTGTGTCAGACCATCTCTGCCCCCAGTGGGAGTGGTCA 2034
3220 TCATGTTCTAAGACCTGTGGGAAGGGTTTACAAAAA 3256
2035 TCATGTTCTAAGACCTGTGGGAAGGGTTTACAAAAA 2071

RESULT 6
US-09-513-999C-32662
; Sequence 32662, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32662
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 259
OTHER INFORMATION: k=g or t
US-09-513-999C-32662

Query Match 1.7%; Score 67; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 1.6e-22;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3653 TACAAGTTTGAAGAAACAAAGCAATTTGCAAAAAAGTTAGAACTATTACAAACCCCTGC 3712
DB 1 TACAAGTTTGAAGAAACAAAGCAATTTGCAAAAAAGTTAGAACTATTACAAACCCCTGT 60
QY 3713 TTCTCTGGTACTTATCAATACTTAGTATCATCGGGGTTGGGAAATGAAAGTAGGAGA 3770
DB 61 TTCTCTGGTACTTATCAATACTTAGTATCATCGGGGTTGGGAAATGAAAGTAGGAGA 118

RESULT 7
US-09-445-023A-13
Sequence 13, Application US/09445023A
Patent No. 6565858

GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiichi
APPLICANT: Hakoziaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical composition and method of immunologically analyzing human ADAMTS

FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445, 023A

CURRENT FILING DATE: 1999-12-03

PRIOR FILING DATE: JP 9-160422

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.0

SEQ ID NO 13

LENGTH: 2184

TYPE: DNA

ORGANISM: Mus sp.

FEATURE:

NAME/KEY: exon

LOCATION: (1)..(2184)

US-09-445-023A-13

Query Match 0.9%; Score 38; DB 4; Length 2184;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2566 TGTGATCGCATCATGACTCCAAAAAGAGTTTGATAA 2603
DB 1381 TGTGATCGCATCATGACTCCAAAAAGAGTTTGATAA 1418

RESULT 8

US-09-445-023A-14
Sequence 14, Application US/09445023A
Patent No. 6565858

GENERAL INFORMATION:

APPLICANT: Hirose, Kunitaka

APPLICANT: Inoguchi, Eiichi

APPLICANT: Hakoziaki, Michinori

APPLICANT: Ishioka, Keiko

APPLICANT: Ishida, Yukako

APPLICANT: Matsushima, Kouji

APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical composition and method of immunologically analyzing human ADAMTS

FILE REFERENCE: Q57092

CURRENT APPLICATION NUMBER: US/09/445, 023A

CURRENT FILING DATE: 1999-12-03

PRIOR FILING DATE: JP 9-160422

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.0

SEQ ID NO 14

LENGTH: 303

TYPE: DNA

ORGANISM: Homo sapiens

US-09-445-023A-14

Query Match 0.8%; Score 34; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2415 TGGCGTCTCACAAGGACAGGTGCAAGCTCATC 2448
DB 240 TGGCGTCTCACAAGGACAGGTGCAAGCTCATC 273

RESULT 9

US-09-063-743-2

Sequence 2, Application US/09063743

Patent No. 6242214

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Guegler, Karl J.

APPLICANT: Corley, Neil C.

APPLICANT: Patterson, Chandra

TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/063,743

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0508 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGNOT01

CLONE: 059953

US-09-063-743-2

Query Match 0.7%; Score 29; DB 3; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGGTCCGCCACGGCTCCGGCGGC 29
DB 1 CCCACGGTCCGCCACGGCTCCGGCGGC 29

RESULT 10

US-09-590-540-2

Sequence 2, Application US/09590540

Patent No. 6410267

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Lal, Preeti

Guegler, Karl J.

Corley, Neil C.

Patterson, Chandra

TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Genomics, Inc.

STREET: 3160 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/590,540

FILING DATE: 08-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/063,743

FILING DATE: April 21, 1998

ATTORNEY/AGENT INFORMATION:

NAME: David G. Streeter

REGISTRATION NUMBER: 43,168

REFERENCE/DOCKET NUMBER: PF-0508-1 DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGN0T01

CLONE: 059953

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-590-540-2

Query Match 0.7%; Score 29; DB 3; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGGTCCGCCACGGCTCCGGCGGC 29
DB 1 CCCACGGTCCGCCACGGCTCCGGCGGC 29

RESULT 11

US-09-205-258-239

Sequence 239, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 239
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-239

Query Match 0.7%; Score 28; DB 4; Length 1250;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCACGGTCCGCCACCGCTCCGCGG 28
Db 2 CCCACGGTCCGCCACCGCTCCGCGG 29

RESULT 12

US-09-205-258-166
; Sequence 166, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
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; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,916
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-166

Query Match 0.7%; Score 28; DB 4; Length 1251;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCACGGTCCGCCACCGCTCCGCGG 28
Db 2 CCCACGGTCCGCCACCGCTCCGCGG 29

RESULT 13

US-09-150-460B-9
; Sequence 9, Application US/09150460B
; Patent No. 6190882
; GENERAL INFORMATION:
; APPLICANT: Lee, Cheng-Chi
; APPLICANT: Albrecht, Urs

APPLICANT: Eichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhythm-Like Gene
FILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 9
LENGTH: 4700
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Nucleotide sequence of m-rigui, a murine brain cDNA
OTHER INFORMATION: homologous to a human RIGUI 4.7 cDNA probe
US-09-150-460B-9

Query Match .0.7%; Score 28; DB 3; Length 4700;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 28
DB 9 CCCACGCGTCCGCCACGCGTCCGGCGG 36

RESULT 14
US-09-620-312D-68
Sequence 68, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 68
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (76)..(1665)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1956)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-68

Query Match 0.7%; Score 27; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 27
DB 17 CCCACGCGTCCGCCACGCGTCCGGCGG 43

RESULT 15
US-09-311-689B-25
Sequence 25, Application US/09311689B
Patent No. 6800726
GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
APPLICANT: Roesler, Keith
TITLE OF INVENTION: Proteins With Enhanced Levels of
TITLE OF INVENTION: Essential Amino Acids
FILE REFERENCE: 0571R2
CURRENT APPLICATION NUMBER: US/09/311,689B
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 08/740,682
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/US97/20441
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 428
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(303)
US-09-311-689B-25

Query Match 0.6%; Score 26; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 26
DB 4 CCCACGCGTCCGCCACGCGTCCGGCGG 29

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Job time : 663 secs

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 13:41:07 ; Search time 2115 Seconds
(without alignments)

11638.363 Million cell updates/sec

Title: US-09-373-658C-125

Perfect score: 4014

Sequence: 1 cccacgctccgcccacgcg.....cttttggaccactccag 4014

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 5695437 seqs, 3066160638 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4014	100.0	4014	11	US-09-989-687-125
2	3147	78.4	4014	16	US-10-115-286-1
3	3147	78.4	4014	18	US-10-757-450-1
4	2922	72.8	4676	13	US-10-105-929-1
5	2871	71.5	4760	10	US-09-971-429B-17
6	2672	66.6	4447	18	US-10-755-889-133
7	2570	64.0	4459	17	US-10-159-563-192
8	2570	64.0	4459	17	US-10-159-563-308
9	2548	63.5	3430	18	US-10-473-974-98
10	2471	61.6	3889	19	US-10-667-281-1
11	2463	61.4	4352	19	US-10-741-600-776

12	2463	61.4	4658	19	US-10-741-600-775	Sequence 775, App
13	2443	60.9	4309	16	US-10-210-120-57	Sequence 57, Appl
14	2329	58.0	3261	10	US-09-373-658-1	Sequence 1, Appl
15	2329	58.0	3261	11	US-09-989-687-1	Sequence 1, Appl
16	2213	55.1	4459	19	US-10-741-600-777	Sequence 777, App
17	1506	37.5	4848	17	US-10-425-114-26851	Sequence 26851, A
18	1443	35.9	3147	9	US-09-803-589-1	Sequence 1, Appl
19	1443	35.9	3147	18	US-10-718-332-1	Sequence 1, Appl
20	1303	32.5	2184	9	US-09-445-023A-2	Sequence 2, Appl
21	1303	32.5	2184	14	US-10-097-597-2	Sequence 2, Appl
22	1303	32.5	2184	14	US-10-097-580-2	Sequence 2, Appl
23	1008	25.1	2134	10	US-09-887-527-23	Sequence 23, Appl
24	1005	25.0	2121	9	US-09-818-143-15	Sequence 15, Appl
25	787	19.6	21130	19	US-10-741-600-17789	Sequence 17789, A
26	506	12.6	506	16	US-10-029-386-22939	Sequence 22939, A
27	467	11.6	569	16	US-10-029-386-9236	Sequence 9236, Ap
28	466	11.6	475	10	US-09-373-658-105	Sequence 105, App
29	466	11.6	475	11	US-09-989-687-105	Sequence 105, App
30	336	9.9	527	19	US-10-696-639-2878	Sequence 2678, Ap
31	331	9.7	504	16	US-10-029-386-11612	Sequence 11612, A
32	389	9.7	632	10	US-09-373-658-103	Sequence 103, App
33	389	9.7	632	11	US-09-989-687-103	Sequence 103, App
34	358	8.9	481	15	US-10-106-698-3692	Sequence 3692, Ap
35	346	8.6	485	17	US-10-242-535A-33817	Sequence 33817, A
36	346	8.6	485	17	US-10-085-783A-33817	Sequence 33817, A
37	315	7.8	519	10	US-09-373-658-104	Sequence 104, App
38	315	7.8	519	11	US-09-989-687-104	Sequence 104, App
39	312	7.8	542	10	US-09-373-658-14	Sequence 14, Appl
40	312	7.8	542	11	US-09-989-687-14	Sequence 14, Appl
41	309	7.7	320	10	US-09-373-658-15	Sequence 15, Appl
42	309	7.7	320	10	US-09-373-658-109	Sequence 109, App
43	309	7.7	320	11	US-09-989-687-15	Sequence 15, Appl
44	309	7.7	320	11	US-09-989-687-109	Sequence 109, App
45	301	7.5	539	16	US-10-029-386-4132	Sequence 4132, Ap

ALIGNMENTS

RESULT 1

US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Hastings, Gregg A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.10700D
; CURRENT APPLICATION NUMBER: US/09/989, 687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (456)..(3366)
; OTHER INFORMATION:
US-09-989-687-125

Query Match 100.0%; Score 4014; DB 11; Length 4014;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCACGCGTCCGCCACGCGTCCGGCGGCTCCGAGCAGGGGCTATTGCAAGCCAGGT 60
Db 1 CCCACGCGTCCGCCACGCGTCCGGCGGCTCCGAGCAGGGGCTATTGCAAGCCAGGT 60
Qy 61 GCCTACCGACGAGGAGGAGCCCTGAGCAGTGTGACACATCGCAGCCAGCG 120
Db 61 GCCTACCGACGAGGAGGAGCCCTGAGCAGTGTGACACATCGCAGCCAGCG 120

QY 121 GAGCGGAGAGGGGCGCAGGACCAATCTCGGGTTCCTCAGCCCGGAGGCGCCCC 180
DB 121 GAGGCGAAGAGGGGCGCAGGACCAATCTCGGGTTCCTCAGCCCGGAGGCGCCCC 180
QY 181 AGAGCGCTTCTTGTCCAGCAGAGGACACTCTCGCTCGCGCTCGCTCTCAGTGTCTCCAA 240
DB 181 AGAGCGCTTCTTGTCCAGCAGAGGACACTCTCGCTCGCGCTCGCTCTCAGTGTCTCCAA 240
QY 241 TTTGGCGTGGAGAGAAAATCTCCGCGCGCCGGCAGAACTGACGCGCTCTCTTTAGTGA 300
DB 241 TTTGGCGTGGAGAGAAAATCTCCGCGCGCCGGCAGAACTGACGCGCTCTCTTTAGTGA 300
QY 301 CTCGCGAGCTTCGGCTGTAGCGGCTGTGCGGCGCTTCCAAAGAAATAGAAATGT 360
DB 301 CTCGCGAGCTTCGGCTGTAGCGGCTGTGCGGCGCTTCCAAAGAAATAGAAATGT 360
QY 361 TAAATTTAAATCCAGAGCAGGACCAAGAGGCTTGTCTCCGACCCGAACTAAAGCT 420
DB 361 TAAATTTAAATCCAGAGCAGGACCAAGAGGCTTGTCTCTCCGACCCGAACTAAAGCT 420
QY 421 CCTCGCTCCGCTCGCTGTCTAGCGGCTGTCTCTGGGGCTCCAAATGACGAGCTGTG 480
DB 421 CCTCGCTCCGCTCGCTGTCTAGCGGCTGTCTCTGGGGCTCCAAATGACGAGCTGTG 480
QY 481 CCGAGGGGTTCCGAGAGGCGAGCTGGCGGAGGACATGGGGAACGCGAGGGGCTCG 540
DB 481 CCGAGGGGTTCCGAGAGGCGAGCTGGCGGAGGACATGGGGAACGCGAGGGGCTCG 540
QY 541 GGGTCTCGGAGCTTTGGGCGCGTACCCAGCTGTCTCTCGCGCGGCGCTACTGGCC 600
DB 541 GGGTCTCGGAGCTTTGGGCGCGTACCCAGCTGTCTCTCGCGCGGCGCTACTGGCC 600
QY 601 GTGTGCGACGCTCGGGCGCGCTCCGAGGAGGACGAGGAGCTAGTGTGCGGAGCTG 660
DB 601 GTGTGCGACGCTCGGGCGCGCTCCGAGGAGGACGAGGAGCTAGTGTGCGGAGCTG 660
QY 661 GAGCGGTTCCGGGACACGGGACCGCGCTCCGCTCGAGCTTCAGCTCCAGAACGCTG 720
DB 661 GAGCGGTTCCGGGACACGGGACCGCGCTCCGCTCGAGCTTCAGCTCCAGAACGCTG 720
QY 721 GATCTGGAGCTGCGCGCCGACAGAGCTTTTGGGCGCGGCTTCAGCTCCAGAACGCTG 780
DB 721 GATCTGGAGCTGCGCGCCGACAGAGCTTTTGGGCGCGGCTTCAGCTCCAGAACGCTG 780
QY 781 GGGCGAAATCCGGGTCGACACCGCTTCCGGAAACCGAAGCTGCGCACTGCTTCTAC 840
DB 781 GGGCGAAATCCGGGTCGACACCGCTTCCGGAAACCGAAGCTGCGCACTGCTTCTAC 840
QY 841 TCGGCGACCTGATGGCGATCCAGCTCGGCTCGCGCTCAGCTCTGCGAGGGCGTG 900
DB 841 TCGGCGACCTGATGGCGATCCAGCTCGGCTCGCGCTCAGCTCTGCGAGGGCGTG 900
QY 901 CGCGCGCTTCTACCTGTGGGGAGGCGTATTTTCATCAGCGCTGCGCGCGCGCAGC 960
DB 901 CGCGCGCTTCTACCTGTGGGGAGGCGTATTTTCATCAGCGCTGCGCGCGCGCAGC 960
QY 961 GAGCGCTCGCACAACCGCGCGCGAGGAGAGCGCGCGCGCAGCTACAGTTTCCACCTC 1020
DB 961 GAGCGCTCGCACAACCGCGCGCGAGGAGAGCGCGCGCGCAGCTACAGTTTCCACCTC 1020
QY 1021 CTGCGCGGAATCGGCGAGGCGAGCTAGCGGCGAGCTGCGGGTCTGAGCAGCGAGCC 1080
DB 1021 CTGCGCGGAATCGGCGAGGCGAGCTAGCGGCGAGCTGCGGGTCTGAGCAGCGAGCC 1080
QY 1081 CGCGCGCTGGGAAACCGGAGACCGAAGACGAGGAGCTGAGGGGCGAGGAGCGAA 1140
DB 1081 CGCGCGCTGGGAAACCGGAGACCGAAGACGAGGAGCTGAGGGGCGAGGAGCGAA 1140
QY 1141 GGGCTCTAGTGTGCGCGGAGGACCGGCGAGCTGCAAGGGGTGAGGACGCGGAGCT 1200
DB 1141 GGGCTCTAGTGTGCGCGGAGGACCGGCGAGCTGCAAGGGGTGAGGACGCGGAGCT 1200

QY 1201 GGAACATAAGAAAGCGATTTGTGTCCAGTCCAGCTATGTGGAACCATGCTTGTG 1260
DB 1201 GGAACATAAGAAAGCGATTTGTGTCCAGTCCAGCTATGTGGAACCATGCTTGTG 1260
QY 1261 GCAGACCAAGTCCAGTGGCAGAAATCCACGGCAGTGTCTAAAGCATTA CTTCTCACTG 1320
DB 1261 GCAGACCAAGTCCAGTGGCAGAAATCCACGGCAGTGTCTAAAGCATTA CTTCTCACTG 1320
QY 1321 TTTTCGGTGGCAGCCAGATTTGTAACAAACACCCAGCATTCGTAATTCAGTTAGCTG 1380
DB 1321 TTTTCGGTGGCAGCCAGATTTGTAACAAACACCCAGCATTCGTAATTCAGTTAGCTG 1380
QY 1381 GTGGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCGGAGTGCACCTCCAA 1440
DB 1381 GTGGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCGGAGTGCACCTCCAA 1440
QY 1441 GCGCTCACTCTGCGGAACTTTTGCACCTGGCAGAGCAGCAACCCACCCAGTGACCG 1500
DB 1441 GCGCTCACTCTGCGGAACTTTTGCACCTGGCAGAGCAGCAACCCACCCAGTGACCG 1500
QY 1501 GATGAGAGCACTATGACACAGCAATTTCTTTTCCAGACAGGACTTGTGGTCCCG 1560
DB 1501 GATGAGAGCACTATGACACAGCAATTTCTTTTCCAGACAGGACTTGTGGTCCCG 1560
QY 1561 ACATGTGATCTCTTGGGATGGCTGATGTGGAACTGTGTGTGATCCGAGCAGAACTG 1620
DB 1561 ACATGTGATCTCTTGGGATGGCTGATGTGGAACTGTGTGTGATCCGAGCAGAACTG 1620
QY 1621 TCCGTCATAGAGATGATGGTTTACAAGTGCCTTCAACAGCCCATGAATTAGGCCAC 1680
DB 1621 TCCGTCATAGAGATGATGGTTTACAAGTGCCTTCAACAGCCCATGAATTAGGCCAC 1680
QY 1681 GTGTTTAACTGCAATGATGATGCAAGAGTGTGCGAGCTTAAATGGTGTGAACCG 1740
DB 1681 GTGTTTAACTGCAATGATGATGCAAGAGTGTGCGAGCTTAAATGGTGTGAACCG 1740
QY 1741 GATTCGCCCATGATGGCGTCAATGTCTTCCAACTGGACCAAGCCAGCTTGTGCTCT 1800
DB 1741 GATTCGCCCATGATGGCGTCAATGTCTTCCAACTGGACCAAGCCAGCTTGTGCTCT 1800
QY 1801 TGCACTGCTACATGATTAATCATCTTCTGGATAATGCTCATGGGGAATGTTGATG 1860
DB 1801 TGCACTGCTACATGATTAATCATCTTCTGGATAATGCTCATGGGGAATGTTGATG 1860
QY 1861 AGCTCTGAGATCCCATACAGCTCCAGCGATCTCCCTGGCAGCTTGTGATGCGCAC 1920
DB 1861 AGCTCTGAGATCCCATACAGCTCCAGCGATCTCCCTGGCAGCTTGTGATGCGCAC 1920
QY 1921 CGGCACTGCTAGTTTACATTTTGGGAGGAGTCCAAACACTGCTGATGACCGAGCACA 1980
DB 1921 CGGCACTGCTAGTTTACATTTGGGAGGAGTCCAAACACTGCTGATGACCGAGCACA 1980
QY 1981 TGTAGCACTTGTGTGTACCGGCACTCTGTTGGGGTGTCTGGTGTGTCAAAACCAAC 2040
DB 1981 TGTAGCACTTGTGTGTACCGGCACTCTGTTGGGGTGTCTGGTGTGTCAAAACCAAC 2040
QY 2041 TTTCCGTTGGCGGATGGCACCAGCTGTGAGGAAATGTTGATCAACGGCAGTGT 2100
DB 2041 TTTCCGTTGGCGGATGGCACCAGCTGTGAGGAAATGTTGATCAACGGCAGTGT 2100
QY 2101 GTGAAACAAACCAACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAA 2160
DB 2101 GTGAAACAAACCAACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAA 2160
QY 2161 GGGCTTGGGAGACTGTTTCGAGAACTGTCGGTGTGAGGAGTCCAGTACAGTATGAGG 2220
DB 2161 GGGCTTGGGAGACTGTTTCGAGAACTGTCGGTGTGAGGAGTCCAGTACAGTATGAGG 2220
QY 2221 TGTGACAAACCACTCCAAAGAACTGTAAGGAACTGTGTAAGGAAACAGTGTGCTAC 2280
DB 2221 TGTGACAAACCACTCCAAAGAACTGTAAGGAACTGTGTAAGGAAACAGTGTGCTAC 2280
QY 2281 AGATCTGTAACTTTGAGGAGTGTCCAGACAAATAATGGAACAACTTTTAGAGAGGAA 2340

Db 2281 AGATCTGTAACTTGGAGCTGTCCAGACAAATAATGGAACACCTTTAGAGAGAACAA 2340
Qy 2341 TGTGAAGCACAACAAGCTTTTCAAAAGCTTCTTTGGAGTGGGCTCGCGTGGATGG 2400
Db 2341 TGTGAAGCACAACAAGCTTTTCAAAAGCTTCTTTGGAGTGGGCTCGCGTGGATGG 2400
Qy 2401 ATTCCCAAGTACGCTGGCGTCTCCACAAAGCAGAGTGCATCTGCGCCAAAGCAAA 2460
Db 2401 ATTCCCAAGTACGCTGGCGTCTCCACAAAGCAGAGTGCATCTGCGCCAAAGCAAA 2460
Qy 2461 GGCATTGGCTACTCTTCTGGTTTGGAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCA 2520
Db 2461 GGCATTGGCTACTCTTCTGGTTTGGAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCA 2520
Qy 2521 GATTCCACCTCTGTCTGTGTCAGGACAGTGTGTAAGCTGTTGTGATCGCATCATY 2580
Db 2521 GATTCCACCTCTGTCTGTGTCAGGACAGTGTGTAAGCTGTTGTGATCGCATCATY 2580
Qy 2581 GACTCCAAAAGAAAGTTTGAATAATGTGTGTTTGGCGGGGAAATGGATCTACTTGTAAA 2640
Db 2581 GACTCCAAAAGAAAGTTTGAATAATGTGTGTTTGGCGGGGAAATGGATCTACTTGTAAA 2640
Qy 2641 AAAATATCAGGATCAGTTACTGTGCAAAACCTGGAATATCATGATATCATCAATTTCCA 2700
Db 2641 AAAATATCAGGATCAGTTACTGTGCAAAACCTGGAATATCATGATATCATCAATTTCCA 2700
Qy 2701 ACTGGAGCCACCAACATCGAAGTGAACACGCGGAAACAGAGGGGATCCAGGAACAATGGC 2760
Db 2701 ACTGGAGCCACCAACATCGAAGTGAACACGCGGAAACAGAGGGGATCCAGGAACAATGGC 2760
Qy 2761 AGCTTTCTCCCATCAAAAGCTGTGTGTCAGGACATATATCTTAATGGTGACTACACTTTG 2820
Db 2761 AGCTTTCTCCCATCAAAAGCTGTGTGTCAGGACATATATCTTAATGGTGACTACACTTTG 2820
Qy 2821 TCCACCTTTAGGACGACATATATGTAACAAGTGTGTCTTGTAGGTACAGCGGCTCTCT 2880
Db 2821 TCCACCTTTAGGACGACATATATGTAACAAGTGTGTCTTGTAGGTACAGCGGCTCTCT 2880
Qy 2881 GCGGCATTTGAAGAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGGACCATCCAGTT 2940
Db 2881 GCGGCATTTGAAGAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGGACCATCCAGTT 2940
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Db 2941 CTCTAGTGGGCAATGCCCTTGCACCTTAAATATACACCTACTTCTGTAAGAAGAAAG 3000
Qy 3001 AAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGAGTGGGGCGAA 3060
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Qy 3061 TGTCTTAAGTCATGTGAATTTGGTGTGTCAGAGAGACTGTGTAAGTCCCGAGACATTAAT 3120
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Qy 3121 GGCAGCTCTCTCCAGTGTGCAAGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3180
Db 3121 GGCAGCTCTCTCCAGTGTGCAAGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3180
Qy 3181 GACCATCCCTGCCCCAGTGGGAGTGGTCAATCATGTCTTAAAGACCTGTGGG 3240
Db 3181 GACCATCCCTGCCCCAGTGGGAGTGGTCAATCATGTCTTAAAGACCTGTGGG 3240
Qy 3241 AAGGTTACAAAAACAGCTTGAAGTGTCTGTCATGATGAGGGGGTGTATCTCAT 3300
Db 3241 AAGGTTACAAAAACAGCTTGAAGTGTCTGTCATGATGAGGGGGTGTATCTCAT 3300
Qy 3301 GACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCAATTTTCAATTTTCAATTTTCA 3360
Db 3301 GACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCAATTTTCAATTTTCAATTTTCA 3360
Qy 3361 TGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGAGGGGCAAGGCAAGTGGAGGAGGCTG 3420

Db 3361 TGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGAGGGCAAGCAAGTGGAGGAGGCTG 3420
Qy 3421 GTGCAGGAAAGCAAGAGCTGGAGGATCCAGCGTATCTTCCAGTAAACAGTGGGT 3480
Db 3421 GTGCAGGAAAGCAAGAGCTGGAGGATCCAGCGTATCTTCCAGTAAACAGTGGGT 3480
Qy 3481 GTATCAGTAAAGTGGGATTTATGGGGGTAGATAGAAAAGGATTTGAATCATCAGAGTAAAC 3540
Db 3481 GTATCAGTAAAGTGGGATTTATGGGGGTAGATAGAAAAGGATTTGAATCATCAGAGTAAAC 3540
Qy 3541 TGCAGTTCGCAATTTTATAGAGTATGTAGTGGAGTATTAACCTCTCAGAGTGTATAT 3600
Db 3541 TGCAGTTCGCAATTTTATAGAGTATGTAGTGGAGTATTAACCTCTCAGAGTGTATAT 3600
Qy 3601 AGCATATTAAGCCCGGCGCATTTATTAATTTTCTTTTGTTCATCTACTACAGTT 3660
Db 3601 AGCATATTAAGCCCGGCGCATTTATTAATTTTCTTTTGTTCATCTACTACAGTT 3660
Qy 3661 TAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTACACCCCTCTCTCTGTT 3720
Db 3661 TAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTACACCCCTCTCTCTGTT 3720
Qy 3721 ACTTATCAATACCTTATAGTATCATGGGGTGGGAAATGAAAAGTAGGAGAAAAGTGGAT 3780
Db 3721 ACTTATCAATACCTTATAGTATCATGGGGTGGGAAATGAAAAGTAGGAGAAAAGTGGAT 3780
Qy 3781 TTTTACTAAGACCTGTTTTTACTTTTACCTCACTAAACAATGGGGGAGAAAGAGTACAAAT 3840
Db 3781 TTTTACTAAGACCTGTTTTTACTTTTACCTCACTAAACAATGGGGGAGAAAGAGTACAAAT 3840
Qy 3841 AGATCTTTTGCAGACACTGTTTTATGGGCTGCTATGGTTTTCAGAGAACGTCTATACAT 3900
Db 3841 AGATCTTTTGCAGACACTGTTTTATGGGCTGCTATGGTTTTCAGAGAACGTCTATACAT 3900
Qy 3901 ATTTCTACCGAGATTTAAACCTTCAGATTTTCCAAATGAGAGGAAAGGCTCAGGC 3960
Db 3901 ATTTCTACCGAGATTTAAACCTTCAGATTTTCCAAATGAGAGGAAAGGCTCAGGC 3960
Qy 3961 AAGTGGAAATACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCCAG 4014
Db 3961 AAGTGGAAATACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCCAG 4014

RESULT 2

US-10-115-286-1

; Sequence 1, Application US/10115286

; Publication No. US20030166065A1

; GENERAL INFORMATION:

; APPLICANT: Jonak, Zdenka

; Trulli, Stephen

; Fornwald, James

; Terrett, Jonathan

; Hastings, Gregg

TITLE OF INVENTION: No. US20030166065A1e1 Integrin Ligand ITGL-TSP

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/115,286

FILING DATE: 04-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/845,496

filed date
present

/	FILING DATE: <Unknown>
/	ATTORNEY/AGENT INFORMATION:
/	NAME: Prestia, Paul F
/	REGISTRATION NUMBER: 23,031
/	REFERENCE/DOCKET NUMBER: GH-70000
/	TELECOMMUNICATION INFORMATION:
/	TELEPHONE: 610-407-0700
/	TELEFAX: 610-407-0701
/	TELEX: 846169
/	INFORMATION FOR SEQ ID NO: 1:
/	SEQUENCE CHARACTERISTICS:
/	LENGTH: 4014 base pairs
/	TYPE: nucleic acid
/	STRANDEDNESS: single
/	TOPOLOGY: linear
/	MOLECULE TYPE: cDNA
/	SEQUENCE DESCRIPTION: SEQ ID NO: 1:
/	US-10-115-286-1

Query Match		78.4%;	Score 3147;	DB 16;	Length 4014;
Best Local Similarity		99.6%;	Pred. No. 0;		
Matches 3997;		Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0

QY	1	CCACAGCGTCCGCCCAACGCTCCGGCGCTCCGAGCCAGGGGCTATTCCAAAGCCAGGGT	60
Db	1	CCCAAGCGTCCGCCCAACGCTCCGGCGCTCCGAGCCAGGGGCTATTCCAAAGCCAGGGT	60
QY	61	GCGCTACCGGACGGAGAGGGGAGAGCCTTGAGCAGAGTGAGCAACATCGCAGCCAAAGCG	120
Db	61	GCGCTACCGGACGGAGAGGGGAGAGCCTTGAGCAGAGTGAGCAACATCGCAGCCAAAGCG	120
QY	121	GAGGCCAAGAGGGCGGCAGGCACCATACTCCGGTTGGCTTCAGCCCCGGAGGCGCCCC	180
Db	121	GAGGCCAAGAGGGCGGCAGGCACCATACTCCGGTTGGCTTCAGCCCCGGAGGCGCCCC	180
QY	181	AGAGCGTTCTTGTCCAGCAGAGCACTGTGCTGCGCCTGCCTCTCAGTGTCCTCCAAC	240
Db	181	AGAGCGTTCTTGTCCAGCAGAGCACTGTGCTGCGCCTGCCTCTCAGTGTCCTCCAAC	240
QY	241	TTTTCGCTGGAGAAGAAAACTTCCCGCGCGCGGAGACTCGAGCGCTCTCTTAGTGA	300
Db	241	TTTTCGCTGGAGAAGAAAACTTCCCGCGCGCGGAGAACTCGAGCGCTCTCTTAGTGA	300
QY	301	CTCCGGAGCTTCGGCTGTAGCGCTCTGCGCGCCTTCCAAACGAAATAAGAAATGT	360
Db	301	CTCCGGAGCTTCGGCTGTAGCGCTCTGCGCGCCTTCCAAACGAAATAAGAAATGT	360
QY	361	TAAATTTAAACAATCCAGCAGAGGCAACAGAGCTTTGTCTCCCGACCCGAACTAAAGCT	420
Db	361	TAAATTTAAACAATCCAGCAGAGGCAACAGAGCTTTGTCTCCCGACCCGAACTAAAGCT	420
QY	421	CCCTCGCTCCGTGCGCTGCTACGAGCGGTGTCTCTGGGGCTCCAATCGACGAGCTGTG	480
Db	421	CCCTCGCTCCGTGCGCTGCTACGAGCGGTGTCTCTGGGGCTCCAATCGACGAGCTGTG	480
QY	481	CCCAGAGGGTTCCGAAAGCGCAAGCTGGGACGACATGGGGAAACGGAGCGGGCTCCG	540
Db	481	CCCAGAGGGTTCCGAAAGCGCAAGCTGGGACGACATGGGGAAACGGAGCGGGCTCCG	540
QY	541	GGGTCTCGGAGCTTTGGGCCCGTAACCAACGTGTGTGTCTCGCGCGCGCGCTACTGCCC	600
Db	541	GGGTCTCGGAGCTTTGGGCCCGTAACCAACGTGTGTGTCTCGCGCGCGCGCTACTGCCC	600
QY	601	GTGTCCGACGCACTCGGGCGCCCTCCGAGGAGACGAGGAGTAGTGGTCCGAGCTG	660
Db	601	GTGTCCGACGCACTCGGGCGCCCTCCGAGGAGACGAGGAGTAGTGGTCCGAGCTG	660
QY	661	GAGCGCGTCCCGGACACGGGACACAGCGCTCCGCTGACGCTTTGACCCAGCAGCTG	720
Db	661	GAGCGCGCTCCCGGACACGGGACACAGCGCTCCGCTGACGCTTTGACCCAGCAGCTG	720
QY	721	GATCTGACGTCGCCCGCGACAGCAGCTTTTTTGGCGCCCGCGCTTCCAGCTCCAGAACGTG	780

Qy	1861	AAGCCTCAGAAATCCCATACAGCTCCCGAGGCGATCTCCCTGGGCACTCTGTTACGATGCCAAC	1920
Db	1861	AAGCCTCAGAAATCCCATACAGCTCCCGAGGCGATCTCCCTGGGCACTCTGTTACGATGCCAAC	1920
Qy	1921	CGCAGTCGCAGATTACATTTGGGGAGGACTCCAAACACATGCCCTGATGCAGCCAGCAC	1980
Db	1921	CGGCAGTCGCAGATTACATTTGGGGAGGACTCCAAACACATGCCCTGATGCAGCCAGCAC	1980
Qy	1981	TGTAGCACCTTTGTGTGTACCGGCACCTCTGTGTGGGTGCTGGTGTCTCAAAACCAACAC	2040
Db	1981	TGTAGCACCTTTGTGTGTACCGGCACCTCTGTGTGGGTGCTGGTGTCTCAAAACCAACAC	2040
Qy	2041	TTCCCGTGGGGGATGGCACAGCTGTGGAGAGGGGAAATGGTGTATCAACGGCAGTAGTGT	2100
Db	2041	TTCCCGTGGGGGATGGCACAGCTGTGGAGAGGGGAAATGGTGTATCAACGGCAGTAGTGT	2100
Qy	2101	GTGAACAAAAACACACAGAAAGCATTTTGTATACGGCTTTTTCATGGAGCTGGCGAAATGTGG	2160
Db	2101	GTGAACAAAAACCGACAGAAAGCATTTTGTATACGGCTTTTTCATGGAGCTGGCGAAATGTGG	2160
Qy	2161	GGGCTTTGGGGAGACTGTTTCAGAGAACGTGCGGTGGAGAGTCCAGTACACGATGAGGGAA	2220
Db	2161	GGGCTTTGGGGAGACTGTTTCAGAGAACGTGCGGTGGAGAGTCCAGTACACGATGAGGGAA	2220
Qy	2221	TGTGACAAACCGAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGCAACAGATGCGCTAC	2280
Db	2221	TGTGACAAACCGAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGCAACAGATGCGCTAC	2280
Qy	2281	AGATCCTGTAACTTTGAGGACTGTCCAGACAAATAATGGAAGAAACCTTTTACAGAGGAACAA	2340
Db	2281	AGATCCTGTAACTTTGAGGACTGTCCAGACAAATAATGGAAGAAACCTTTTACAGAGGAACAA	2340
Qy	2341	TGTGAAGCACACAAACGAGTTTTCAAAAGCTTTCCTTTGGGAGTGGGCTCGGGTGGAAATGG	2400
Db	2341	TGTGAAGCACACAAACGAGTTTTCAAAAGCTTTCCTTTGGGAGTGGGCTCGGGTGGAAATGG	2400
Qy	2401	ATTCCCAAGTACCGCTGGCGTCTACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAA	2460
Db	2401	ATTCCCAAGTACCGCTGGCGTCTACCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAA	2460
Qy	2461	GGCATTCGGCTACTTCTTCCTTTGCGCTTTCGAGCCCAAGGTGTAGATGGTATCCTCATGTAGCCCA	2520
Db	2461	GGCATTCGGCTACTTCTTCCTTTGCGCTTTCGAGCCCAAGGTGTAGATGGTATCCTCATGTAGCCCA	2520
Qy	2521	GATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAGCTGGTGTGATTCGATCATTA	2580
Db	2521	GATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAGCTGGTGTGATTCGATCATTA	2580
Qy	2581	GACTCCAAAAGAGTTTGATAATGTGGTGTGCGGGGGAATGATCTACTTGTAAA	2640
Db	2581	GACTCCAAAAGAGTTTGATAATGTGGTGTGCGGGGGAATGATCTACTTGTAAA	2640
Qy	2641	AAAATATCAGGATCAGTTACTAGTGTGCAAAACCTGGATATCATGATATCATCAAAATTCGA	2700
Db	2641	AAAATATCAGGATCAGTTACTAGTGTGCAAAACCTGGATATCATGATATCATCAAAATTCGA	2700
Qy	2701	ACTGGAGCCACCAACATCGAAGTGAACACAGCGGAACAGAGGGGATCCAGGAACAATGGC	2760
Db	2701	ACTGGAGCCACCAACATCGAAGTGAACACAGCGGAACAGAGGGGATCCAGGAACAATGGC	2760
Qy	2761	AGCTTTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAATGTGACTACACTTTG	2820
Db	2761	AGCTTTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAATGTGACTACACTTTG	2820
Qy	2821	TCCACCTTAGAGCAAGCAATTAATGTAACAAAGGTGTGTCTTTGAGGTACAGCGGTCTCTCT	2880
Db	2821	TCCACCTTAGAGCAAGCAATTAATGTAACAAAGGTGTGTCTTTGAGGTACAGCGGTCTCTCT	2880
Qy	2881	GCGGCATTTGGAAGAAATTCGCAGCTTTAGCGCTCTCAAGAGCCCTTGAACAATCCAGGTT	2940
Db	2881	GCGGCATTTGGAAGAAATTCGCAGCTTTAGCGCTCTCAAGAGCCCTTGAACAATCCAGGTT	2940

QY	2941	CTTACTGTGGGCAATGCCCTTTCGACCTTAAATATTAACACCTTACTTCTGTAAGAAGAAG	3000
DB	2941	CTTACTGTGGGCAATGCCCTTTCGACCTTAAATATTAACACCTTACTTCTGTAAGAAGAAG	3000
QY	3001	AAGGAATCTTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAA	3060
DB	3001	AAGGAATCTTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAA	3060
QY	3061	TGTTCTTAAGTCATGTGAAATTTGGGTGGCAGAGAAGACTGTTAGAAATGCCGAGACATTAAT	3120
DB	3061	TGTTCTTAAGTCATGTGAAATTTGGGTGGCAGAGAAGACTGTTAGAAATGCCGAGACATTAAT	3120
QY	3121	GGCAGCGCTGCTTCCGAGTGTGCAAAAGGAAGTGAAGCCAGCCAGCAGCACGACCTTGTGCA	3180
DB	3121	GGCAGCGCTGCTTCCGAGTGTGCAAAAGGAAGTGAAGCCAGCCAGCAGCACGACCTTGTGCA	3180
QY	3181	GACCATCCCTGCCCGCAGTGGCAGTGGGGAGTGGTTCATCATGTCTTAAGACCTGTGGG	3240
DB	3181	GACCATCCCTGCCCGCAGTGGCAGTGGGGAGTGGTTCATCATGTCTTAAGACCTGTGGG	3240
QY	3241	AAGGGTTACAAAAAACAAGCTTGAAGTGTCTGTCCCACATCATGAGGGGTGTATCTCAT	3300
DB	3241	AAGGGTTACAAAAAAGAAGCTTGAAGTGTCTGTCCCACATCATGAGGGGTGTATCTCAT	3300
QY	3301	GACAGCTGTGATCCCTTTTAAAGAAACCTTAAACATTTTCATAGACTTTTGCACAAATGGCGAA	3360
DB	3301	GAGAGCTGTGATCCCTTTTAAAGAAACCTTAAACATTTTCATAGACTTTTGCACAAATGGCGAA	3360
QY	3361	TGCAGTTAAGTGGTTTAAGTGGTGTAGCTTTGAGGCAAGCCAAAGTAGGAGAGGCTG	3420
DB	3361	TGCAGTTAAGTGGTGTAGTGGTGTAGCTTTGAGGCAAGCCAAAGTAGGAGAGGCTG	3420
QY	3421	GTGCAGGGAAGCAAGAAAGCTGGAGGGAATCCAGCGTATCTTCCAGTAACCAAGTGAAGT	3480
DB	3421	GTGCAGGGAAGCAAGAAAGCTGGAGGGAATCCAGCGTATCTTCCAGTAACCAAGTGAAGT	3480
QY	3481	GTATCAGTAAGTGGGATTAATGGGGGTAGATAGAAAAAGGAGTTGAATCATCAGAGTAAAC	3540
DB	3481	GTATCAGTAAGTGGGATTAATGGGGGTAGATAGAAAAAGGAGTTGAATCATCAGAGTAAAC	3540
QY	3541	TGCCAGTTGCAAATTTTCATAGGATAGTTAGTAGGATTTATTAACCTCTGAGCAGTGAAT	3600
DB	3541	TGCCAGTTGCAAATTTGATAGATAGTTAGTAGGATTTATTAACCTCTGAGCAGTGAAT	3600
QY	3601	AGCATATAAGCCCCCGGCATTATTAATTAATTTCTTTTGTTCATCTACTACAAGTT	3660
DB	3601	AGCATATAAGCCCCCGGCATTATTAATTAATTTCTTTTGTTCATCTACTACAAGTT	3660
QY	3661	TAGAAAAAACAAGCAATTGTCAAAAAAGTTAGAACTATTAACAACCTCTGAGCAGTGAAT	3720
DB	3661	TAGAAAAAACAAGCAATTGTCAAAAAAGTTAGAACTATTAACAACCTCTGAGCAGTGAAT	3720
QY	3721	ACTTATCAAAATACCTAGTATCATGGGGTTGGGAAATGAAAGGTAGGAGAAAAAGTGAAT	3780
DB	3721	ACTTATCAAAATACCTAGTATCATGGGGTTGGGAAATGAAAGGTAGGAGAAAAAGTGAAT	3780
QY	3781	TTTACTAAGACCTGTTTTTACTTTACCTCACTAAACAAATGGGGGAGAAAGGAGTACAAT	3840
DB	3781	TTTACTAAGACCTGTTTTTACTTTACCTCACTAAACAAATGGGGGAGAAAGGAGTACAAT	3840
QY	3841	AGGATCTTTTTCACAGCAGCTGTTTATGGGCTGCTATGGTTTCAGAGAACTGTATACATT	3900
DB	3841	AGGATCTTTTTCACAGCAGCTGTTTATGGGCTGCTATGGTTTCAGAGAACTGTATACATT	3900
QY	3901	ATTTTCTACCGAGGATTTAAACCTTCCAGATTGTTTCCAACTGGAGAGGAAGGCTCAGGC	3960
DB	3901	ATTTTCTACCGAGGATTTAAACCTTCCAGATTGTTTCCAACTGGAGAGGAAGGCTCAGGC	3960
QY	3961	AACGTGGAAATAACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCCAG	4014
DB	3961	AACGTGGAAATAACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCCAG	4014

RESULT 3

US-10-757-450-1

; Sequence 1, Application US/10757450

; Publication No. US2004017594A1

; GENERAL INFORMATION:

; APPLICANT: Jonak, Zdenka

; Trulli, Stephen

; Fornwald, James

; Terrett, Jonathan

; Hasting, Gregg

; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/757,450

; FILING DATE: 15-Jan-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/10/115,286

; FILING DATE: 04-Apr-2002

; APPLICATION NUMBER: 08/845,496

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Prestia, Paul F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4014 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-757-450-1

Query Match 78.4%; Score 3147; DB 18; Length 4014;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3997; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY	1	CCACGCTCCGCGCTCCGCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGT	60
DB	1	CCACGCTCCGCGCTCCGCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGT	60
QY	61	GGCTACCGGAGGAGGGAGAGCCCTGAGCAGAGTGAGCAACATCGACCAAGGGG	120
DB	61	GGCTACCGGAGGAGGGAGAGCCCTGAGCAGAGTGAGCAACATCGACCAAGGGG	120
QY	121	GAGGCGAAGAGGGGGCCAGGACCAATCTCGGGTTGCCCTCAGCCCGAGGGGGCCC	180
DB	121	GAGGCGAAGAGGGGGCCAGGACCAATCTCGGGTTGCCCTCAGCCCGAGGGGGCCC	180
QY	181	AGAGGCTTTCTTGTCCACAGAGCCACTCTGCTGCGCTCCCTCTCAGTGTCTCCAC	240
DB	181	AGAGGCTTTCTTGTCCACAGAGCCACTCTGCTGCGCTCCCTCTCAGTGTCTCCAC	240
QY	241	TTTTCGGTGGAGAAAAAATTTCCGCGCGCCGCGAGAACTGACGCGCTCTCTTAGTGA	300
DB		TTTTCGGTGGAGAAAAAATTTCCGCGCGCCGCGAGAACTGACGCGCTCTCTTAGTGA	300

DB	241	TTTTCGGTGGAGAAAAAATTTCCGCGCGCCGCGAGAACTGACGCGCTCTCTTAGTGA	300
QY	301	CTTCGCGGAGCTTCGGCTGTAGCCGGCTCTGCGCGCCCTTCCAAAGAAATTAATAAATTT	360
DB	301	CTTCGCGGAGCTTCGGCTGTAGCCGGCTCTGCGCGCCCTTCCAAAGAAATTAATAAATTT	360
QY	361	TAAATTTTAACTCCAGAGCAGGCAACAGAGCTTTTGTCTCCCGACCCGAACTAAAGCT	420
DB	361	TAAATTTTAACTCCAGAGCAGGCAACAGAGCTTTTGTCTCTCCCGACCCGAACTAAAGCT	420
QY	421	CCCTCGCTCCGTCGCTGTACAGCGGTGTCTCTCTGGGGCTCCCAATGACAGCGAGCTGTG	480
DB	421	CCCTCGCTCCGTCGCTGTACAGCGGTGTCTCTCTGGGGCTCCCAATGACAGCGAGCTGTG	480
QY	481	CCGAGGGGTTCCGAAAGCGCAAGCTGGGACGCAATGGGGAAACGCGAGCGGGCTCCG	540
DB	481	CCGAGGGGTTCCGAAAGCGCAAGCTGGGACGCAATGGGGAAACGCGAGCGGGCTCCG	540
QY	541	GGGTCTCGGAGCTTTGGGCGCGGTACCCAGCTGTCTGCTCGCGCGCGCTACTTGGCC	600
DB	541	GGGTCTCGGAGCTTTGGGCGCGGTACCCAGCTGTCTGCTCGCGCGCGCTACTTGGCC	600
QY	601	GTGTCGAGCGCACTCGGGCGCCCTTCGAGGAGGACGAGAGCTAGTGTGCGCGAGCTG	660
DB	601	GTGTCGAGCGCACTCGGGCGCCCTTCGAGGAGGACGAGAGCTAGTGTGCGCGAGCTG	660
QY	661	GAGCGGCTCCGCGGACAGCGGCTCTCCGCTGCGAGCTTTGACACGAGCTGTG	720
DB	661	GAGCGGCTCCGCGGACAGCGGCTCTCCGCTGCGAGCTTTGACACGAGCTGTG	720
QY	721	GATCTGGAGCTGCGCGCGCGACAGAGCTTTTGGGCGCGCGCTTCCAGCTTCAGAACCTG	780
DB	721	GATCTGGAGCTGCGCGCGCGACAGAGCTTTTGGGCGCGCGCTTCCAGCTTCAGAACCTG	780
QY	781	GGGCGCAATCCGGTCCGACACCCCGCTTCGGAACCGACCTCGCGCTCTCTTCTAC	840
DB	781	GGGCGCAATCCGGTCCGACACCCCGCTTCGGAACCGACCTCGCGCTCTCTTCTAC	840
QY	841	TCCGCGAGTGGGATGCGGATCCAGCTCGGCTGCGCGCTCAGCTCTGCGAGGGCGTG	900
DB	841	TCCGCGAGTGGGATGCGGATCCAGCTCGGCTGCGCGCTCAGCTCTGCGAGGGCGTG	900
QY	901	CGCGCGCTTCTACTCTGCGGGAGGCTATTTCATCAGCCGCTGCGCGCGCGCTG	960
DB	901	CGCGCGCTTCTACTCTGCGGGAGGCTATTTCATCAGCCGCTGCGCGCGCGCTG	960
QY	961	GAGCGCTCGCACCGCGCGCGCGAGGAGAGCGCGCGCACCACTACAGTTCCACCTC	1020
DB	961	GAGCGCTCGCACCGCGCGCGCGAGGAGAGCGCGCGCACCACTACAGTTCCACCTC	1020
QY	1021	CTGCGCGGATCCGAGGCGGACGTAGCGCGGACGTGGGGTCTGTGACGACGAGGCC	1080
DB	1021	CTGCGCGGATCCGAGGCGGACGTAGCGCGGACGTGGGGTCTGTGACGACGAGGCC	1080
QY	1081	CGGCGCACTGGGAAAGCGGAGACCGAAGACGAGGAGGAGCTGAGGGCGAGGACGAA	1140
DB	1081	CGGCGCACTGGGAAAGCGGAGACCGAAGACGAGGAGGAGCTGAGGGCGAGGACGAA	1140
QY	1141	GGGCTCTAGTGGTCCCGCAGGACCCCGCACTGCAAGGCTAGGACAGCCACAGAACT	1200
DB	1141	GGGCTCTAGTGGTCCCGCAGGACCCCGCACTGCAAGGCTAGGACAGCCACAGAACT	1200
QY	1201	GGAAGCATAGAAAGAGGATTTGTGTCAGTCCCGCTATGTGGAACCATGCTTGTG	1260
DB	1201	GGAAGCATAGAAAGAGGATTTGTGTCAGTCCCGCTATGTGGAACCATGCTTGTG	1260
QY	1261	GAGACCACTGATGGCAGAAATTCACGCGAGTGTCTAAAGCATTTACCTTCTCAGTTG	1320
DB	1261	GAGACCACTGATGGCAGAAATTCACGCGAGTGTCTAAAGCATTTACCTTCTCAGTTG	1320
QY	1321	TTTTTCGGTGGAGCAAGATTGTGAACAAACCCAGCATTCGTAATTCAGTAGCCCTGTG	1380
DB	1321	TTTTTCGGTGGAGCAAGATTGTGAACAAACCCAGCATTCGTAATTCAGTAGCCCTGTG	1380

Qy	1381	GTGGTGAAGATCTTTGGTCA	TCCAGATGAACAGAGGGG	CCGAGTGACCTCCAATGCT	1440
Db	1381	GTGGTGAAGATCTTTGGTCA	TCCAGATGAACAGAGGGG	CCGAGTGACCTCCAATGCT	1440
Qy	1441	GCCTCACTCTGGGAACTTTT	GGCACTGGCAGAGCAAC	CCCATGACCGG	1500
Db	1441	GCCTCACTCTGGGAACTTTT	GGCACTGGCAGAGCAAC	CCCATGACCGG	1500
Qy	1501	GATGCAGACATATGACACAG	CAATCTCTTTTCCACAG	CAGACATGTGTGGGTCCCAG	1560
Db	1501	GATGCAGACATATGACACAG	CAATCTCTTTTCCACAG	CAGACATGTGTGGGTCCCAG	1560
Qy	1561	ACATGTGATACTCTTGGGAT	GGCTGATTTGGAACTCTGT	GTGTGATCCGAGCAAGACTGC	1620
Db	1561	ACATGTGATACTCTTGGGAT	GGCTGATTTGGAACTCTGT	GTGTGATCCGAGCAAGACTGC	1620
Qy	1621	TCCGTCAAGAAGATAGTTTA	CAAGCTGCCTTCCACAC	CAGCCATGAATTAGGCCAC	1680
Db	1621	TCCGTCAAGAAGATAGTTTA	CAAGCTGCCTTCCACAC	CAGCCATGAATTAGGCCAC	1680
Qy	1681	GTGTTTAAACATGCCATGAT	GTGAAAGCAGTGTGCCAG	CTTAATGTGTGAACCCAG	1740
Db	1681	GTGTTTAAACATGCCATGAT	GTGAAAGCAGTGTGCCAG	CTTAATGTGTGAACCCAG	1740
Qy	1741	GATTCCCAATGATGGCGTCA	ATGTCTTCCAACTCGACCA	CAGCCAGCTTCGTCTCCT	1800
Db	1741	GATTCCCAATGATGGCGTCA	ATGTCTTCCAACTCGACCA	CAGCCAGCTTCGTCTCCT	1800
Qy	1801	TGCAGTGGCTACATGATTA	CATCATTTCTGGATAATGG	TATGGGAAATTTTGTATGGAC	1860
Db	1801	TGCAGTGGCTACATGATTA	CATCATTTCTGGATAATGG	TATGGGAAATTTTGTATGGAC	1860
Qy	1861	AGCCTCAGAAATCCCATAC	AGCTCCAGGCGATCTCCCT	GGCAGCTCTGTACGATGCCAC	1920
Db	1861	AGCCTCAGAAATCCCATAC	AGCTCCAGGCGATCTCCCT	GGCAGCTCTGTACGATGCCAC	1920
Qy	1921	CGGCAGTGCAGATTTCAT	TTTGGGGAGCACTCCAAAC	ACTGCCCTGATGCAGCCAGCACA	1980
Db	1921	CGGCAGTGCAGATTTCAT	TTTGGGGAGCACTCCAAAC	ACTGCCCTGATGCAGCCAGCACA	1980
Qy	1981	TGTAGCACCTTGTGGTGTAC	CGGCACCTCTGTGGGGTGT	CTGGTGTCAAAACAAACAC	2040
Db	1981	TGTAGCACCTTGTGGTGTAC	CGGCACCTCTGTGGGGTGT	CTGGTGTCAAAACAAACAC	2040
Qy	2041	TTCCCGTGGGGGATGGCA	CCAGCTGTGGAGAGGGAAAT	TGGTGTATCAACGGCAAGTGT	2100
Db	2041	TTCCCGTGGGGGATGGCA	CCAGCTGTGGAGAGGGAAAT	TGGTGTATCAACGGCAAGTGT	2100
Qy	2101	GTGAACAAAACACACAGAA	AGCATTTTGTATACGCTTTT	TCATGGAAGCTGGGGAATGTGG	2160
Db	2101	GTGAACAAAACACACAGAA	AGCATTTTGTATACGCTTTT	TCATGGAAGCTGGGGAATGTGG	2160
Qy	2161	GGGCTTTGGGAGACTGTTC	CGAGAACGTGGGTGGAGAGT	TCCAGTACACGATGAGGAA	2220
Db	2161	GGGCTTTGGGAGACTGTTC	CGAGAACGTGGGTGGAGAGT	TCCAGTACACGATGAGGAA	2220
Qy	2221	TGTGACAAACCCAGTCCCAA	AGATGGAGGGAAGTACTGT	GAGCAAAACAGTGCCTAC	2280
Db	2221	TGTGACAAACCCAGTCCCAA	AGATGGAGGGAAGTACTGT	GAGCAAAACAGTGCCTAC	2280
Qy	2281	AGATCTGTATACCTTTGAG	GAAGTGTCCAGACAAATAAT	TGAAACCTTTAGAGAGAACAA	2340
Db	2281	AGATCTGTATACCTTTGAG	GAAGTGTCCAGACAAATAAT	TGAAACCTTTAGAGAGAACAA	2340
Qy	2341	TGTGAAGCACAAACGAGTTT	TCAAAAGCTTCTTTTGGG	AGTGGGCTCGCGGTGAATGG	2400
Db	2341	TGTGAAGCACAAACGAGTTT	TCAAAAGCTTCTTTTGGG	AGTGGGCTCGCGGTGAATGG	2400
Qy	2401	ATTCCCAAGTACGTGGCGT	CTCCAAAGGACAGGTGCA	AGTCTATCTGCCAAGCCAAA	2460
Db	2401	ATTCCCAAGTACGTGGCGT	CTCCAAAGGACAGGTGCA	AGTCTATCTGCCAAGCCAAA	2460

Qy	2461	GGCATTGGCTACTCTTCTTGTTTTGAGACCCCAAGTTGTAGATGGTACTCATTGATGCCCA	2522
Db	2461	GGCATTGGCTACTCTTCTTGTTTTGAGACCCCAAGTTGTAGATGGTACTCATTGATGCCCA	2520
Qy	2521	GATTTCCACCTCTCTGCTGTGCAAGGACAGTGTGTAAAGCTGTTGTGATCCCATCATYA	2580
Db	2521	GATTTCCACCTCTCTGCTGTGCAAGGACAGTGTGTAAAGCTGTTGTGATCCCATCATYA	2580
Qy	2581	GACTTCCAAAAGAAGTTTGATAAATGTGTGTTTTGCGGGGAAATGATCTACTTTGTAAA	2640
Db	2581	GACTTCCAAAAGAAGTTTGATAAATGTGTGTTTTGCGGGGAAATGATCTACTTTGTAAA	2640
Qy	2641	AAAATATCAGGATCAGTTACTAGTGTGAAAACCTCTGGATATCATGATATCATCACAATTCCA	2700
Db	2641	AAAATATCAGGATCAGTTACTAGTGTGAAAACCTCTGGATATCATGATATCATCACAATTCCA	2700
Qy	2701	ACTGGAGCCACCAACATCGAAGTGTAAACACGCGAAACAGAGGGGATCCAGAAACAATGGC	2760
Db	2701	ACTGGAGCCACCAACATCGAAGTGTAAACACGCGAAACAGAGGGGATCCAGAAACAATGGC	2760
Qy	2761	AGCTTTCTTGCCCATCAAAGCTGCTGATGGCACATATATCTTAAATGGTGACTACCTTTG	2820
Db	2761	AGCTTTCTTGCCCATCAAAGCTGCTGATGGCACATATATCTTAAATGGTGACTACCTTTG	2820
Qy	2821	TCCACCTTAGAGCAAGACATATATGTAACAAGTGTGTCTTGAGGTTACACGGCTCCTCT	2880
Db	2821	TCCACCTTAGAGCAAGACATATATGTAACAAGTGTGTCTTGAGGTTACACGGCTCCTCT	2880
Qy	2881	CGGCGATTGAAAGNATTCGACGTTTTCAGCCCTCTCAAGAGCGCTTGACCATCCAGGTT	2940
Db	2881	CGGCGATTGAAAGNATTCGACGTTTTCAGCCCTCTCAAGAGCGCTTGACCATCCAGGTT	2940
Qy	2941	CTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAATACACTACTTCTGTTAAAGAGAAG	3000
Db	2941	CTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAATACACTACTTCTGTTAAAGAGAAG	3000
Qy	3001	AAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAA	3060
Db	3001	AAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAA	3060
Qy	3061	TGTTCTTAAGTCATGTGAATTTGGGTTCGCAGAGAGACTGGTGTAGAAATGCCAGACATTAAT	3120
Db	3061	TGTTCTTAAGTCATGTGAATTTGGGTTCGCAGAGAGACTGGTGTAGAAATGCCAGACATTAAT	3120
Qy	3121	GGACAGCTGCTTCCGAGTGTGCAAGGAAGTGAAGCCAGCAGCACCAAGACCTTTGTGCA	3180
Db	3121	GGACAGCTGCTTCCGAGTGTGCAAGGAAGTGAAGCCAGCAGCACCAAGACCTTTGTGCA	3180
Qy	3181	GACCATCCCTGCCCAAGTGGGAGTGGTTCATCATGTTCTAAGACCTGTGGG	3240
Db	3181	GACCATCCCTGCCCAAGTGGGAGTGGTTCATCATGTTCTAAGACCTGTGGG	3240
Qy	3241	AAGGGTTACAAAACCAAGCTTGAAGTGTCTGCCATGATGGAGGGGTATCTCAT	3300
Db	3241	AAGGGTTACAAAACCAAGCTTGAAGTGTCTGCCATGATGGAGGGGTATCTCAT	3300
Qy	3301	GACAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTATAGACTTTTGCACAATGGCAGAA	3360
Db	3301	GACAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTATAGACTTTTGCACAATGGCAGAA	3360
Qy	3361	TGCAGTTAAGTGGTTTAAGTGGTTAGCTTTGAGGCGAAGGCAAGTGTAGAGAGGGCTG	3420
Db	3361	TGCAGTTAAGTGGTTTAAGTGGTTAGCTTTGAGGCGAAGGCAAGTGTAGAGAGGGCTG	3420
Qy	3421	GTGAGGGAAAGCAAGAGCTTGAGGGATCCAGCGTATCTTCCAGTAAACAGTGAAGT	3480
Db	3421	GTGAGGGAAAGCAAGAGCTTGAGGGATCCAGCGTATCTTCCAGTAAACAGTGAAGT	3480
Qy	3481	GTATCAGTAAGTGGGATTTATGGGGGTAGATAGAAAAGGAGTGTGAATCATCAGAGTAAAC	3540
Db	3481	GTATCAGTAAGTGGGATTTATGGGGGTAGATAGAAAAGGAGTGTGAATCATCAGAGTAAAC	3540
Qy	3541	TGCCAGTTTGCAAAATTTTGTATAGGATAGTGTAGTGAGGATTTATTAACCTCTGACAGTGTAT	3600

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Db 3541 TCCAGTTCCTCAATTTGATAGATAGTATTAGTGGAGTATTAACTCTGAGCAGTAT 3600
QY 3601 AGCATATAAAGCCCGGCATTAATTAATTAATTTCTTTGTTACATCTACTCAAGTT 3660
Db 3601 AGCATATAAAGCCCGGCATTAATTAATTAATTTCTTTGTTACATCTACTCAAGTT 3660
QY 3661 TAGAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTATTACAACTCTGCTCTGTT 3720
Db 3661 TAGAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTATTACAACTCTGTTCTGTT 3720
QY 3721 ACTTATCAATACTTAGTATCATGCGGTTGGGAAATGAAAGTAGAGGAAAGTGAGAT 3780
Db 3721 ACTTATCAATACTTAGTATCATGCGGTTGGGAAATGAAAGTAGAGGAAAGTGAGAT 3780
QY 3781 TTTTACTAAGACCTGTTTACTTTTACTTCTACTTAACTTCCAACTAGGAGGAAAGTGAGAT 3840
Db 3781 TTTTACTAAGACCTGTTTACTTTTACTTCTACTTAACTTCCAACTAGGAGGAAAGTGAGAT 3840
QY 3841 AGGATCTTTTGAACAGCAGCTGTTTATGGGCTGCTATGTTTTCAGAGAACTTATACATT 3900
Db 3841 AGGATCTTTTGAACAGCAGCTGTTTATGGGCTGCTATGTTTTCAGAGAACTTATACATT 3900
QY 3901 ATTTCTACCGAGGATTTAAACTTCCAGATTTGTTCCAACTAGGAGGAAAGTGAGAT 3960
Db 3901 ATTTCTACCGAGGATTTAAACTTCCAGATTTGTTCCAACTAGGAGGAAAGTGAGAT 3960
QY 3961 AACGTGGAATAACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCAG 4014
Db 3961 AACGTGGAATAACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCAG 4014

RESULT 4
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-10-105-929-1

Query Match 72.8%; Score 2922; DB 13; Length 4676;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3772; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 25 GCGGCTCCGAGCCAGGGGCTATTGCAAGCCAGGGTGCCTACCGGACGGAGGGGAGA 84
Db 19 GCGGCTCCGAGCCAGGGGCTATTGCAAGCCAGGGTGCCTACCGGACGGAGGGGAGA 78
QY 85 GCGCTGAGCAGAGTGAACAATCGCAGCAAGGGCGAGCCGCAAGAGGGCGCCAGGCA 144
Db 79 GCGCTGAGCAGAGTGAACAATCGCAGCAAGGGCGAGCCGCAAGAGGGCGCCAGGCA 138
QY 145 CCAATCTCCGCTGTGCTCAGCCCCCGAGGCGCCCCCAGAGCGCTTTTGTCCAGCAGAG 204
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Db 139 CCAATCTCCGCTGTGCTCAGCCCCCGAGGCGCCCCCAGAGCGCTTTCTTGTCCAGCAGAG 198
QY 205 CCACCTCTGCTGCGCTCGCTCTCAGTGTCTCAAACTTTTGGCTGGAAGAAAACCTTCCC 264
Db 199 CCACCTCTGCTGCGCTCGCTCTCAGTGTCTCAAACTTTTGGCTGGAAGAAAACCTTCCC 258
QY 265 GCGGCGCGGCAAGACTGCGAGCGCTCTCTTAGTGACCTCCGAGAGCTTTCGGCTGTAGCGG 324
Db 259 GCGGCGCGGCAAGACTGCGAGCGCTCTCTTAGTGACCTCCGAGAGCTTTCGGCTGTAGCGG 318
QY 325 GCTCTGCGCGCTTCTCCAACTGAAATTAAGAAATTTGTTAAATTTTAACTTCCAGAGCAGGC 384
Db 319 GCTCTGCGCGCTTCTCCAACTGAAATTAAGAAATTTGTTAAATTTTAACTTCCAGAGCAGGC 378
QY 385 CAAAGAGGCTTTGCTCTCCGAGCCGCAATTAAGCTCCCTCGCTCGCTGCTGCTGCTACGA 444
Db 379 CAAAGAGGCTTTGCTCTCCGAGCCGCAATTAAGCTCCCTCGCTCGCTGCTGCTGCTACGA 438
QY 445 GCGGTGTCTCTTGGGGCTTCCAACTGAGCAGCTGTGCGGAGGGTTCGGAAGGCGCAAG 504
Db 439 AGGCTGTCTCTTGGGGCTTCCAACTGAGCAGCTGTGCGGAGGGTTCGGAAGGCGCAAG 498
QY 505 CTGGGACGCAATCGGGAACCGCGAGCGGCTCCGGGTTCTCGAGCTTTTGGGCCCCGTA 564
Db 499 CTGGGACGCAATCGGGAACCGCGAGCGGCTCCGGGTTCTCGAGCTTTTGGGCCCCGTA 558
QY 565 CCAAGCTGTGCTGCTCGCGCGCGCTACTTGGGCGGTTCGGAAGCCTCGGCGCGCCC 624
Db 559 CCAAGCTGTGCTGCTCGCGCGCGCTACTTGGGCGGTTCGGAAGCCTCGGCGCGCCC 618
QY 625 TCCGAGGAGGACGAGAGCTAGTGTGCGGAGCTGAGCGGCTCCCGGACACCGGAGCC 684
Db 619 TCCGAGGAGGACGAGAGCTAGTGTGCGGAGCTGAGCGGCTCCCGGACACCGGAGCC 678
QY 685 AGCGCTCTCGGCTCGACCGCTTTGACGAGCAGCTGGAATCTGGAAGTCCGCGCCGACAGC 744
Db 679 AGCGCTCTCGGCTCGACCGCTTTGACGAGCAGCTGGAATCTGGAAGTCCGCGCCGACAGC 738
QY 745 AGCTTTTGGGCGCGGCTTCAAGCTCCAGAGCTGCGGCGGCAATCCGGTCCGACACC 804
Db 739 AGCTTTTGGGCGCGGCTTCAAGCTCCAGAGCTGCGGCGGCAATCCGGTCCGAGAGC 798
QY 805 CCGCTTCCGGAACCGACCTGCGGCTTCTACTCTCGGACCGCTGAATGGCGATCCC 864
Db 799 CCGCTTCCGGAACCGACCTGCGGCTTCTACTCTCGGACCGCTGAATGGCGATCCC 858
QY 865 AGCTCGGCTGCGGCTTCAAGCTTCTGAGGCGGCTGCGGCGGCTTCTACTGCTGGGG 924
Db 859 AGCTCGGCTGCGGCTTCAAGCTTCTGAGGCGGCTGCGGCGGCTTCTACTGCTGGGG 918
QY 925 GAGGCTATTTCATCCAGCGCTGCGCGCGGAGCGGCTCGCCACCGCGCCGCCA 984
Db 919 GAGGCTATTTCATCCAGCGCTGCGCGCGGAGCGGCTCGCCACCGCGCCGCCA 978
QY 985 GGGGAGAAAGCCCGGACCCACTACAGTTTCCACCTCTCGCGCGGAACTCGGAGGCGGAC 1044
Db 979 GGGGAGAAAGCCCGGACCCACTACAGTTTCCACCTCTCGCGCGGAACTCGGAGGCGGAC 1038
QY 1045 GTAGCGGCACTGCGGGTCTGGAAGCAGAGCGGCTCGGCGGCTGGAAGCGGAGAC 1104
Db 1039 GTAGCGGCACTGCGGGTCTGGAAGCAGAGCGGCTCGGCGGCTGGAAGCGGAGAC 1098
QY 1105 GAAAGCAGGAGCGAAGGACTGAGGCGGAGGAGGAGGCTTCTAGTGTGCTGCGCGGAGGAC 1164
Db 1099 GAAAGCAGGAGCGAAGGACTGAGGCGGAGGAGGAGGCTTCTAGTGTGCTGCGCGGAGGAC 1158
QY 1165 CCGGCACTGCAAGCGGTAGGACAGCCCGAGGAACTGGAAGCATAAGAAAGCGATTT 1224
Db 1159 CCGGCACTGCAAGCGGTAGGACAGCCCGAGGAACTGGAAGCATAAGAAAGCGATTT 1218
QY 1225 GTGTCTCAGTCCGCTATGTGGAACCAATGCTTGTGGCAGCAGCTCGATGCGAGATTC 1284
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QY 3445 AGGGATCCAGCGTATCTTTCCAGTAACCAAGTCCAGTGGTGTATCAGTAAGTGGGATTTATGGG 3504
Db 3439 AGGGATCCAGCGTATCTTTGCCAGTAACCAAGTCCAGTGGTGTATCAGTAAGTGGGATTTATGGG 3498
QY 3505 GGTAGATGAAAGAGTTGAATCATCAGAGTAACCTCCAGTTCGCAAAATTTGATAGGAT 3564
Db 3499 GGTAGATGAAAGAGTTGAATCATCAGAGTAACCTCCAGTTCGCAAAATTTGATAGGAT 3558
QY 3565 AGTTAGTGAGGATTTAATCACTCTCAGCAGTGCATATAGCATATAAAGCCCGGSCATTA 3624
Db 3559 AGTTAGTGAGGATTTAATCACTCTCAGCAGTGCATATAGCATATAAAGCCCGGSCATTA 3618
QY 3625 TTATTTATTTCTTTTGTGTACATCTACTACAAGTTTATAGAAAAAACAAGCAATTTGTCAA 3684
Db 3619 TTATTTATTTCTTTTGTGTACATCTACTACAAGTTTATAGAAAAAACAAGCAATTTGTCAA 3678
QY 3685 AAAAGTTAGAACTATTACAACCCCTGCTTCCTGTACTTATCAAAATCTTAGTATCATG 3744
Db 3679 AAAAGTTAGAACTATTACAACCCCTGCTTCCTGTACTTATCAAAATCTTAGTATCATG 3738
QY 3745 GGGGTTGGGAATGAAAGTAGGAGAAAGTGAGATTTTACTAAGACCTGTTTACTTTTA 3804
Db 3739 GGGGTTGGGAATGAAAGTAGGAGAAAGTGAGATTTTACTAAGACCTGTTTACTTTTA 3798
QY 3805 CCTCACTAA 3813
Db 3799 CCTCACTAA 3807

RESULT 5
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
;
;
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Query Match 71.5%; Score 2871; DB 10; Length 4760;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3771; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 GCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGTGGCTTACCGGACGGAGGGGAGA 84
Db 120 GCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGTGGCTTACCGGACGGAGGGGAGA 179
QY 85 GCGCTGAGCAGAGTGAACAACATCCAGCCAGGCGGAGGCGCAAGAGAGGGGCGCCAGGCA 144
Db 180 GCGCTGAGCAGAGTGAACAACATCCAGCCAGGCGGAGGCGCAAGAGAGGGGCGCCAGGCA 239
QY 145 CCAATCTCGGCTTGGCTTCAGCCCCGAGGGCGCCGACAGCGCTTCTTGTCACAGAG 204
Db 240 CCAATCTCGGCTTGGCTTCAGCCCCGAGGGCGCCGACAGCGCTTCTTGTCACAGAG 299
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QY 205 CCACTCTCCCTCGCGCTCGCTCTCAGTGTCTCAACTTTTGGCTGGAAGAAAACTTCCC 264
Db 300 CCACTCTCCCTCGCGCTCGCTCTCAGTGTCTCAACTTTTGGCTGGAAGAAAACTTCCC 359
QY 265 GCGGCGCGGAGAACTGACGAGCGCTCTCTTTAGTAGACTCCGGGAGCTTCGGCTGAGCGG 324
Db 360 GCGGCGCGGAGAACTGACGAGCGCTCTCTTTAGTAGACTCCGGGAGCTTCGGCTGAGCGG 419
QY 325 GCTCTGCGGCGCTTCCAAAGTAATAGAAATTTGTTAAATTTTAACTTCCAGACGAGC 384
Db 420 GCTCTGCGGCGCTTCCAAAGTAATAGAAATTTGTTAAATTTTAACTTCCAGACGAGC 479
QY 385 CAAAGAGCTTTTGTCTCTCCCGACCCGAACTAAAGCTCCCTCGCTCCGTCGCTGCTACGA 444
Db 480 CAAAGAGCTTTTGTCTCTCCCGACCCGAACTAAAGCTCCCTCGCTCCGTCGCTGCTACGA 539
QY 445 GCGGTGTCTCTGCGGCTTCCAAATGACGAGCTGTGCGGAGGGTTCCGAAAGGCGCAAG 504
Db 540 GCGGTGTCTCTGCGGCTTCCAAATGACGAGCTGTGCGGAGGGTTCCGAAAGGCGCAAG 599
QY 505 CTGGGACGACATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCGCGTA 564
Db 600 CTGGGACGACATGGGGAACGCGGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCGCGTA 659
QY 565 CCCAGCTGTCTGTCTCGCGCGCGCTACTGCGCCGTGTGCGAGCGCACTTCGGGCGCCCC 624
Db 660 CCCAGCTGTCTGTCTCGCGCGCGCTACTGCGCCGTGTGCGAGCGCACTTCGGGCGCCCC 719
QY 625 TCCGAGGAGGACGAGGAGCTAGTGTCCGAGCTGGAGCGGCTCCCGGACACCGGACC 684
Db 720 TCCGAGGAGGACGAGGAGCTAGTGTGCGCGAGCTGGAGCGCGCCCGGACACCGGACC 779
QY 685 AGCGGCTTCCGCTGACGCGCTTTGACCAAGCTGAGTCTGGAGCTGCGGCGCGGACAGC 744
Db 780 AGCGGCTTCCGCTGACGCGCTTTGACCAAGCTGAGTCTGGAGCTGCGGCGCGGACAGC 839
QY 745 AGCTTTTGGCGCGCGCTTCAAGCTCCAGAACGTGGGGCGCAATCCGGGTCCGACACC 804
Db 840 AGCTTTTGGCGCGCGCTTCAAGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGAGC 899
QY 805 CCGCTTCCGAGAAACGACCTCGGCGCATCTGTTCTACTCCGCGACCGTGAATGGCGATCCC 864
Db 900 CCGCTTCCGAGAAACGACCTCGGCGCATCTGTTCTACTCCGCGACCGTGAATGGCGATCCC 959
QY 865 AGCTCGGCTGCGGCGCTTCAGGAGCGGCTGCGGAGGGCGCTTCTACTCTGCTGGG 924
Db 960 AGCTCGGCTGCGGCGCTTCAGGAGCGGCTGCGGAGGGCGCTTCTACTCTGCTGGG 1019
QY 925 GAGGCGTATTTTCATCCAGCGCTGCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCA 984
Db 1020 GAGGCGTATTTTCATCCAGCGCTGCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCA 1079
QY 985 GGGGAGAAAGCCCGGACCACTACAGTTTCACTCTTCGCGCGGAAATCGGAGGGCGAC 1044
Db 1080 GGGGAGAAAGCCCGGACCACTACAGTTTCACTCTTCGCGCGGAAATCGGAGGGCGAC 1139
QY 1045 GTAGCGGCACTGCGGGGTGTTGACCAAGCGCGCGCGGCGGCTGCGGAAAGCGGAGACC 1104
Db 1140 GTAGCGGCACTGCGGGGTGTTGACCAAGCGCGCGCGGCGGCTGCGGAAAGCGGAGACC 1199
QY 1105 GAAAGACGAGGACGAAAGGACTGAGGGCGAGGACGAAAGGGCGCTCAGTGTGCTCGCGCAGGAC 1164
Db 1200 GAAAGACGAGGACGAAAGGACTGAGGGCGAGGACGAAAGGGCGCTCAGTGTGCTCGCGCAGGAC 1259
QY 1165 CCGGCACTGCAAGCGTATAGGACAGCCCAAGGAACTGGAAGCAATAGAAAGAGCGATTT 1224
Db 1260 CCGGCACTGCAAGCGTATAGGACAGCCCAAGGAACTGGAAGCAATAGAAAGAGCGATTT 1319
QY 1225 GTGTCCAGTCAAGCGTATGTAAGCAATGTTGTCAGAGCCAGTCCATGTCAGAAATTC 1284
Db 1320 GTGTCCAGTCAAGCGTATGTAAGCAATGTTGTCAGAGCCAGTCCATGTCAGAAATTC 1379
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Db 3540 AGGGATCCAGCGTATCTTCCAGTAACCACTGAGGTGTATCAGTAAGGTGGGATATGGG 3599
QY 3505 GGTAGATAGAAAAGAGTTGAATCATCAGATTAACCTGCAGTTGCAAAATTTGATAGGAT 3564
Db 3600 GGTAGATAGAAAAGAGTTGAATCATCAGATTAACCTGCAGTTGCAAAATTTGATAGGAT 3659
QY 3565 AGTTAGTGAAGGATTTAACTCTGAGCAGTGTATATAGCATATAAAGCCCGGGCATTA 3624
Db 3660 AGTTAGTGAAGGATTTAACTCTGAGCAGTGTATATAGCATATAAAGCCCGGGCATTA 3719
QY 3625 TTATTATTATTTCTTTTGTGTACATCTACTACAGTTTGTAGAAAAAACAAGCAATTTGTCAA 3684
Db 3720 TTATTATTATTTCTTTTGTGTACATCTACTACAGTTTGTAGAAAAAACAAGCAATTTGTCAA 3779
QY 3685 AAAAGTTAGAACTATTACAAACCTCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 3744
Db 3780 AAAAGTTAGAACTATTACAAACCTCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 3839
QY 3745 GGGGTTGGGAAATGAAAGTGTAGGAGAAAGTGTAGGATTTTACTAAGACCTGTGTTTACTTTTA 3804
Db 3840 GGGGTTGGGAAATGAAAGTGTAGGAGAAAGTGTAGGATTTTACTAAGACCTGTGTTTACTTTTA 3899
QY 3805 CCTCACTAA 3813
Db 3900 CCTCACTAA 3908

RESULT 6
US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Query Match 66.6%; Score 2672; DB 18; Length 4447;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 224 CTCCTAGTCTCTCCAACTTTTGGCTGGAGAGAAAACCTCCCGCGCGCGCGAGAACTGCA 283
Db 1 CTCCTAGTCTCTCCAACTTTTGGCTGGAGAGAAAACCTCCCGCGCGCGCGAGAACTGCA 60
QY 284 GGGCCTCTCTTAGTGACTCCGGAGCTTCGGCTGTAGCGGCTCTGCGCGCCCTTCCAA 343
Db 61 GGGCCTCTCTTAGTGACTCCGGAGCTTCGGCTGTAGCGGCTCTGCGCGCCCTTCCAA 120
QY 344 CGAATAATAGAAATTTGTTAATTTTAAATTCAGATCCAGAGCGGCCAAAGAGCTTTGCTCTCC 403
Db 121 CGAATAATAGAAATTTGTTAATTTTAAATTCAGATCCAGAGCGGCCAGAGGCTTTGCTCTCC 180
QY 404 CGACCCGAACTAAAGTCTCTCGCTCGCTGCTGTAGCGGCTGTCTGAGCGGTGTCTCTGGGGCTC 463
Db 181 CGACCCGAACTAAAGTCTCTCGCTCGCTGCTGTAGCGGCTGTCTGAGCGGTGTCTCTGGGGCTC 240
QY 464 CAATGAGCGAGTGTGCGCGAGGGGTTCGGAAGCGCAAGCTGGCGAGCATGGGGA 523
Db 241 CAATGAGCGAGTGTGCGCGAGGGGTTCGGAAGCGCAAGCTGGCGAGCATGGGGA 300

QY 524 ACGCGAGCGGGCTCGGGGCTCTCGGAGCTTTGGGCGCGGTACCCACGCTGCTGCTGCTCG 583
Db 301 ACGCGAGCGGGCTCGGGGCTCTCGGAGCTTTGGGCGCGGTACCCACGCTGCTGCTGCTCG 360
QY 584 CCGCGCGCTACTGCGCGGTGTCGAGCGACTCGGCGCGCCCTCCGAGGAGGACGAGGAGC 643
Db 361 CCGCGCGCTACTGCGCGGTGTCGAGCGACTCGGCGCGCCCTCCGAGGAGGACGAGGAGC 420
QY 644 TAGTGTGCGGAGTGTGAGCGCGTCCCGGGAACGAGGACGAGCGCTCCCGCTGCGACG 703
Db 421 TAGTGTGCGGAGTGTGAGCGCGCGCCCGGGACACGAGGACGAGCGCTCCCGCTGCGACG 480
QY 704 CTTTGTGACGAGCTGTGATCTGTGAGTGTGCGCGCGCGGACGAGCGCTTTTGGGCGCGCGCT 763
Db 481 CTTTGTGACGAGCTGTGATCTGTGAGTGTGCGCGCGCGGACGAGCGCTTTTGGGCGCGCGCT 540
QY 764 TCACGCTCCAGAACGTTGGGGCGCAATCCGGGTCCGACACCCCGCTTCCGGGAAACCGGAC 823
Db 541 TCACGCTCCAGAACGTTGGGGCGCAATCCGGGTCCGAGCGCGCTTCCGGGAAACCGGAC 600
QY 824 TGGCGCACTGTCTTACTCTCGGCAACGTTGAATGGCGATCCCAAGCTCGGCTGCGCGCTCA 883
Db 601 TGGCGCACTGTCTTACTCTCGGCAACGTTGAATGGCGATCCCAAGCTCGGCTGCGCGCTCA 660
QY 884 GCCTCTGCGAGGGCGTGGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGC 943
Db 661 GCCTCTGCGAGGGCGTGGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGC 720
QY 944 CGCTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCGCCCGCCAGGGAGAACCGCGGAC 1003
Db 721 CGCTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCGCCCGCCAGGGAGAACCGCGGAC 780
QY 1004 CACTACAGTTCCACTCTCTCGGCGGAAATCGGCGAGCGACCTAGGCGGACGCTGCGGG 1063
Db 781 CACTACAGTTCCACTCTCTCGGCGGAAATCGGCGAGCGACCTAGGCGGACGCTGCGGG 840
QY 1064 TCGTGGAGCGAGCGCGCGCGCTGGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGGA 1123
Db 841 TCGTGGAGCGAGCGCGCGCGCGCTGGGAGCGGAGCGGAGCGGAGCGGAGGGA 900
QY 1124 CTGAGGGGAGGAGCGGAGCGCTCAGTGTGCTCCCGCAGGACCGCGCACTGCAAGGCGTAG 1183
Db 901 CTGAGGGGAGGAGCGGAGCGCTCAGTGTGCTCCCGCAGGACCGCGCACTGCAAGGCGTAG 960
QY 1184 GACAGCCACAGGAACTGGAAGCATAAGAAAGCGATTTGTGTCCAGTCAACCGCTATG 1243
Db 961 GACAGCCACAGGAACTGGAAGCATAAGAAAGCGATTTGTGTCCAGTCAACCGCTATG 1020
QY 1244 TGGAAACCATGCTTGTGGCAGACGAGTGTGAGGAGAAATTCACGGCAGTGTCTTAAAGC 1303
Db 1021 TGGAAACCATGCTTGTGGCAGACGAGTGTGAGGAGAAATTCACGGCAGTGTCTTAAAGC 1080
QY 1304 ATTACTCTCTCAGCTGTGTTTTCGGTGGCAGCGAGATTTGACAAACACCCAGCATTCGTA 1363
Db 1081 ATTACTCTCTCAGCTGTGTTTTCGGTGGCAGCGAGATTTGACAAACACCCAGCATTCGTA 1140
QY 1364 ATTACTCTCTCAGCTGTGTTTTCGGTGGCAGCGAGATTTGACAAACACCCAGCATTCGTA 1423
Db 1141 ATTACTCTCTCAGCTGTGTTTTCGGTGGCAGCGAGATTTGACAAACACCCAGCATTCGTA 1200
QY 1424 TAGTCACTCCAACTGCTGCCCTCACTCTCGGAACTTTTGGCAACTGGCAGAGGAGCACA 1483
Db 1201 TAGTCACTCCAACTGCTGCCCTCACTCTCGGAACTTTTGGCAACTGGCAGAGGAGCACA 1260
QY 1484 ACCCAACCCAGTGAACCGGATGACAGGACATATGACACAGCAATTTCTTTTCAACAGAGC 1543
Db 1261 ACCCAACCCAGTGAACCGGATGACAGGACATATGACACAGCAATTTCTTTTCAACAGAGC 1320
QY 1544 ACTTGTGTGGTTCAGACATGTGATACTTTTGGGATGGCTGATGTGGAATCTGTGTGTG 1603
Db 1321 ACTTGTGTGGTTCAGACATGTGATACTTTTGGGATGGCTGATGTGGAATCTGTGTGTG 1380

Qy	1604	ATCCGACGAGAGCTGCTCCGTCAATAGAGATGATGGTTTTAAAGCTGCGCTTCAACACAG	1663
Db	1381	ATCCGACGAGAGCTGCTCCGTCAATAGAGATGATGGTTTTAAAGCTGCGCTTCAACACAG	1440
Qy	1664	CCCATGAATTTAGGCCACGCTGTTTTAAACATGCCATGATGATCAAAAGCAGTGTGCCAGCC	1723
Db	1441	CCCATGAATTTAGGCCACGCTGTTTTAAACATGCCATGATGATGATCAAAAGCAGTGTGCCAGCC	1500
Qy	1724	TTAATGGTGTGAACACGAGGATTCCCAATGATGGCGTCAATGTCTTCCAACTTGACCA	1783
Db	1501	TTAATGGTGTGAACACGAGGATTCCCAATGATGGCGTCAATGTCTTCCAACTTGACCA	1560
Qy	1784	GCAGCGCTTGGTCTCTTTGAGTGGCTACATGATTTATCATCTTTCTGGATATATGTCATG	1843
Db	1561	GCAGCGCTTGGTCTCTTTGAGTGGCTACATGATTTATCATCTTTCTGGATATATGTCATG	1620
Qy	1844	GGGAATTTTGTATGAGCAAGCCCTCAGAACTCCCATACAGCTCCCAAGCGCATCTCCCTGGCA	1903
Db	1621	GGGAATTTTGTATGAGCAAGCCCTCAGAACTCCCATACAGCTCCCAAGCGCATCTCCCTGGCA	1680
Qy	1904	CCTCGTACGATGCCAACCCGCGAGTGGCAGTTTACATTTTGGGGAGGACTCCAAACACTGCC	1963
Db	1681	CCTCGTACGATGCCAACCCGCGAGTGGCAGTTTACATTTTGGGGAGGACTCCAAACACTGCC	1740
Qy	1964	CTGATCAGCCAGCAATGATGACCTTGTGTGTATCCGGCACTCTGTGTGGGTGCTGTG	2023
Db	1741	CTGATCAGCCAGCAATGATGACCTTGTGTGTATCCGGCACTCTGTGTGGGTGCTGTG	1800
Qy	2024	TGTGTCAAAACCAACACTTCCCTGGCGGATGGCACCGACTCTGTGAGAGGAGGAATGTT	2083
Db	1801	TGTGTCAAAACCAACACTTCCCTGGCGGATGGCACCGACTCTGTGAGAGGAGGAATGTT	1860
Qy	2084	GTATCAACGGCAAGTGTGTGAACAAACCAACAGAAAGCAATTTTGATACGCCCTTTTCATG	2143
Db	1861	GTATCAACGGCAAGTGTGTGAACAAACCAACAGAAAGCAATTTTGATACGCCCTTTTCATG	1920
Qy	2144	GAAGCTGGGAAATGTGGGGGCTTTGGGGAGACTGTTCGAGAACTGTCGGTGGAGGAGTCC	2203
Db	1921	GAAGCTGGGAAATGTGGGGGCTTTGGGGAGACTGTTCGAGAACTGTCGGTGGAGGAGTCC	1980
Qy	2204	AGTACAGATGAGGGAATGTGCAACCCAGTCCCAAGAGATGAGAGGAGTACTGTGGAAG	2263
Db	1981	AGTACAGATGAGGGAATGTGCAACCCAGTCCCAAGAGATGAGAGGAGTACTGTGGAAG	2040
Qy	2264	GCAACAGAGTGGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAATAATGGAANA	2323
Db	2041	GCAACAGAGTGGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAATAATGGAANA	2100
Qy	2324	CCTTTAGAGAGGAACAATGTGAAGCAACAACGAGTTTTCAAGCTTCTTTGGGAGTG	2383
Db	2101	CCTTTAGAGAGGAACAATGTGAAGCAACAACGAGTTTTCAAGCTTCTTTGGGAGTG	2160
Qy	2384	GGCTTGGGTGGAATGATTTCCCAAGTACCGTGGCGTCTCAACAAAGGACAGGTGCAAGC	2443
Db	2161	GGCTTGGGTGGAATGATTTCCCAAGTACCGTGGCGTCTCAACAAAGGACAGGTGCAAGC	2220
Qy	2444	TCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTGTTTTGCGCCCAAGTTGTAGATG	2503
Db	2221	TCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTGTTTTGCGCCCAAGTTGTAGATG	2280
Qy	2504	GTACTCCATGTAGCCCAAGATTTCCACTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTG	2563
Db	2281	GTACTCCATGTAGCCCAAGATTTCCACTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTG	2340
Qy	2564	GTTGTGATCGCATCATAGACTCCAAAGAGATTTTGATTAATGTGTGTTTTGCGGGGAA	2623
Db	2341	GTTGTGATCGCATCATAGACTCCAAAGAGATTTTGATTAATGTGTGTTTTGCGGGGAA	2400
Qy	2624	ATGATCTACTTGTGTAAAAAATAATACAGATCAGTTACTAGTGTCAAAACCTTGGATATCATG	2683
Db	2401	ATGATCTACTTGTGTAAAAAATAATACAGATCAGTTACTAGTGTCAAAACCTTGGATATCATG	2460
Qy	2684	ATATCATCACAATTTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAACACAGAGG	2743

2461	Db	ATATCATCAAAATTCNACTGGAGCCACCACATCGAAGTGAACAGCGGACCAGAGGG	2520
2744	Qy	GATCCAGGAACAAATGGCAGCTTTCTTGCCCATCAAAGCTGCTGAATGGCACATATATTCCTTA	2803
2521	Db	GATCCAGGAACAAATGGCAGCTTTCTTGCCCATCAAAGCTGCTGAATGGCACATATATTCCTTA	2580
2804	Qy	ATGGTGACTACACTTTGTTCACCTTAGAGCAAGACATATGTACAAAGTGTTGTCTTGA	2863
2581	Db	ATGGTGACTACACTTTGTTCACCTTAGAGCAAGACATATGTACAAAGTGTTGTCTTGA	2640
2864	Qy	GGTACAGCGGCTCCTCTGGGCAATGCGAAGAAATTCGCAGCTTTAGCCCTCTCAAAAGAGC	2923
2641	Db	GGTACAGCGGCTCCTCTGGGCAATGCGAAGAAATTCGCAGCTTTAGCCCTCTCAAAAGAGC	2700
2924	Qy	CCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATACACCT	2983
2701	Db	CCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATACACCT	2760
2984	Qy	ACTTCGTAAGAAGAAAGGAATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCA	3043
2761	Db	ACTTCGTAAGAAGAAAGGAATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCA	2820
3044	Qy	TTCAAGAGTGGGCGAAATGTTCTTAAGTCAATGTGAAATGGGTGGCAGAGAAGACTGGTAG	3103
2821	Db	TTCAAGAGTGGGCGAAATGTTCTTAAGTCAATGTGAAATGGGTGGCAGAGAAGACTGGTAG	2880
3104	Qy	AATGCCGAGACATTAATGGCAGCCTGCTTCCGAGTGTGCMAAGGAAGTGAAGCCAGCCA	3163
2881	Db	AATGCCGAGACATTAATGGCAGCCTGCTTCCGAGTGTGCMAAGGAAGTGAAGCCAGCCA	2940
3164	Qy	GCACGACACTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCACTCAT	3223
2941	Db	GCACGACACTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCACTCAT	3000
3224	Qy	GTCTAAGACCTGTGGGAAGGGTTACAAAACCAAGCTTGAAGTGTCTGTCCCATGATG	3283
3001	Db	GTCTAAGACCTGTGGGAAGGGTTACAAAACCAAGCTTGAAGTGTCTGTCCCATGATG	3060
3284	Qy	GAGGGGTGTTATCTCATGACAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTATAGACT	3343
3061	Db	GAGGGGTGTTATCTCATGACAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTATAGACT	3120
3344	Qy	TTTGCACAATGGCAGAAATGACAGTTAAGTGGTTAAGTGGTGTAGCTTTTCAGGGCAGGC	3403
3121	Db	TTTGCACAATGGCAGAAATGACAGTTAAGTGGTTAAGTGGTGTAGCTTTTCAGGGCAGGC	3180
3404	Qy	AAAGTCAGGAAGGCTGTGTCAGGGAAAGCAAGAGGCTCGAGGGATCCAGCGTATCTTC	3463
3181	Db	AAAGTCAGGAAGGCTGTGTCAGGGAAAGCAAGAGGCTCGAGGGATCCAGCGTATCTTC	3240
3464	Qy	CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTTATGGGGGTAGATGAAAGGAGTT	3523
3241	Db	CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTTATGGGGGTAGATGAAAGGAGTT	3300
3524	Qy	GAATCATCAGAGTAAACTGCCAGTTCGAAATTTGATAGGATAGTTAGTGAGGATTTATTA	3583
3301	Db	GAATCATCAGAGTAAACTGCCAGTTCGAAATTTGATAGGATAGTTAGTGAGGATTTATTA	3360
3584	Qy	CCTCTGAGCAGTCGATATAGCATTAATAAGCCCGGGCATTTATTTATTTCTTTTGT	3643
3361	Db	CCTCTGAGCAGTCGATATAGCATTAATAAGCCCGGGCATTTATTTATTTCTTTTGT	3420
3644	Qy	TACATCTACTACAAGTTTAGAAAAACAAAGCAATGTCAAAAAAGTTAGAACTATTAC	3703
3421	Db	TACATCTACTACAAGTTTAGAAAAACAAAGCAATGTCAAAAAAGTTAGAACTATTAC	3480
3704	Qy	AACCCCTGCTTCCTGGTACTTATCAAACTATAGTATCATGGGGTGGGAAATGAAAG	3763
3481	Db	AACCCCTGCTTCCTGGTACTTATCAAACTATAGTATCATGGGGTGGGAAATGAAAG	3540
3764	Qy	TAGAGAAAGTGAATTTTACTAAGACCTGTTTTTACTTTTACCTCACTAA	3813

Db 3541 TAGGAGAAAAGTCAGATTTTACTAGACCTGTGTTTACTTTTACTCTACTAA 3590

RESULT 7
US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-192

Query Match 64.0%; Score 2570; DB 17; Length 4459;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3470; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 224 CTTCTAGTCTCTCCAACTTTGGCTGGAGAAAACCTCCCGCGCGCGGAGAACTGCA 283
Db 1 CTTCTAGTCTCTCCAACTTTGGCTGGAGAAAACCTCCCGCGCGCGGAGAACTGCA 60

QY 284 GGGCCCTCTCTTAGTGACTCCGGAGCTTCGGGTGTAGCCGGCTCTGCGCGCCCTTCCAA 343
Db 61 GGGCCCTCTCTTAGTGACTCCGGAGCTTCGGGTGTAGCCGGCTCTGCGCGCCCTTCCAA 120

QY 344 CGAATATAGAAATTTGTTAATTTTAAATCCAGAGAGGCAACAGAGCTTGTCTCC 403
Db 121 CGAATATAGAAATTTGTTAATTTTAAATCCAGAGAGGCAACAGAGCTTGTCTCC 180

QY 404 CGACCCGAACTAAAGTCTCCCTCGCTCGGCGCTGTACAGCGGTGTCTCTGGGGCTC 463
Db 181 CGACCCGAACTAAAGTCTCCCTCGCTCGGCGCTGTACAGCGGTGTCTCTGGGGCTC 240

QY 464 CAATGCAGCGAGCTGTGCCCGAGGGGTTCCGGAAGCGCAAGCTGGGCGACATGGGGA 523
Db 241 CAATGCAGCGAGCTGTGCCCGAGGGGTTCCGGAAGCGCAAGCTGGGCGACATGGGGA 300

QY 524 ACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGGCCGTACCGAGCTGTGCTGCTCG 583
Db 301 ACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGGCCGTACCGAGCTGTGCTGCTCG 360

QY 584 CCGCGCGCTACTGGCCGTGTCGAGCGACTCGGGGCCCTCCGAGGAGGACGAGGAGC 643
Db 361 CCGCGCGCTACTGGCCGTGTCGAGCGACTCGGGGCCCTCCGAGGAGGACGAGGAGC 420

QY 644 TAGTGTGCGGAGCTGGAGCGCGTCCCGGGACACAGGACCCGCTCCGCTGCGACG 703
Db 421 TAGTGTGCGGAGCTGGAGCGCGTCCCGGGACACAGGACCCGCTCCGCTGCGACG 480

QY 704 CTTTGAACAGAGCTGGATCTGGAGCTGCGCGCCGACAGAGCTTTTGGCGCCGGCT 763
Db 481 CTTTGAACAGAGCTGGATCTGGAGCTGCGCGCCGACAGAGCTTTTGGCGCCGGCT 540

QY 764 TCACGCTCCAGAACGTCGGCGCAATCCGGGTCCGACACCCGCTTCCGGAACCGACC 823
Db 541 TCACGCTCCAGAACGTCGGCGCAATCCGGGTCCGAGACCGCGCTTCCGGAACCGACC 600

QY 824 TGGCGCACTGCTTACTCTCGGCACCGTGAATGGCGATCCAGCTCGGCTCGCCCTCA 883

Db 601 TGGCGCACTGCTTACTCTCGGCACCGTGAATGGCGATCCACAGCTCGGCTGCCGCCCTCA 660

QY 884 GCCTCTGGAGGGCGTGGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTATCCACG 943

Db 661 GCCTCTGGAGGGCGTGGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTATCCACG 720

QY 944 CGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCGCCAGGGGAGAGCGCGCGCAC 1003

Db 721 CGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCGCCAGGGGAGAGCGCGCGCAC 780

QY 1004 CACTACAGTTCCACTCTCTGCGCGCGAATCGGACAGGGCGACGTAGCGGCGACGTGCGGG 1063

Db 781 CACTACAGTTCCACTCTCTGCGCGCGAATCGGACAGGGCGACGTTCGCGCGCGACGTGCGGG 840

QY 1064 TCGTGGACGACGAGCCCGCGCGCTGGGAAAGCGAGACCGAAGACGAGGAGGAGGGA 1123

Db 841 TCGTGGACGACGAGCCCGCGCGCTGGGAAAGCGAGACCGAAGACGAGGAGGAGGGA 900

QY 1124 CTGAGGGCGAGGACGAAAGGGCCCTCAGTGTGTCGCCCGCAGGACCCGGCCTTGCAGAGGCGTAG 1183

Db 901 CTGAGGGCGAGGACGAAAGGGCCCTCAGTGTGTCGCCCGCAGGACCCGGCCTTGCAGAGGCGTAG 960

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QY 1364 ATTCAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCCG 1423

Db 1141 ATTCAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCCG 1200

QY 1424 AGTCAGCTCCAACTGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAGAGCAGCA 1483

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Db 1261 ACCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTACCAGACAG 1320

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Db 1321 ACTTGTGTGGTCCCGACATGTGATACTCTTTGGGATGGCTGATGTTGGAACCTGTGTG 1380

QY 1604 ATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGTGCCTTCAACACAG 1663

Db 1381 ATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGTGCCTTCAACACAG 1440

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Db 1501 TTAATGGTGTGAACCGAGATTCCTCCATGATGGCGTCAATGTCTTCCAACTGGACCA 1560

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QY 1904 CTTCTGACGATGCCAACCGGCGAGTCCGATTTTACATTTGGGGAGGAGCTCCAAACACTGCC 1963

Db 1681 CTTCTGACGATGCCAACCGGCGAGTCCGATTTTACATTTGGGGAGGAGCTCCAAACACTGCC 1740

1964 CTGATCAGCCAGCACATGTAGCACCTTGTGTGTATCCGCGACCTCTGTGGGTGCTGG 2023
1741 CCGATCAGCCAGCACATGTAGCACCTTGTGTGTATCCGCGACCTCTGTGGGTGCTGG 1800
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1801 TGTGTCAAAACCAACATCTCCGTGGCGGATGGCACCGAGCTGTGAGAGGGAATGCT 1860
2084 GTATCAACGGCAAGTGTGTGAACAAACACACAGAAAGCATTTGTATACGCTTTTCATG 2143
1861 GTATCAACGGCAAGTGTGTGAACAAACACACAGAAAGCATTTGTATACGCTTTTCATG 1920
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1921 GAAGCTGGGGGAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTCGCGGTGGAGGAGTCC 1980
2204 AGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGATGGAGGAAGTACTGTGAAG 2263
1981 AGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGATGGAGGAAGTACTGTGAAG 2040
2264 GCAACGAGTGGCTACAGATCTGTAAACCTTGAGGACTGTCCAGACAATAATGGAAGAA 2323
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2101 CCTTTAGAGAGGAACAATGTGAAGCACACAACGAGTCTTCAAAAGCTTCTTTGGGAGTG 2160
2384 GGCTCGGTGGGAATGGATTCCTCAAGTACCGTGGCTCTCACAAAGGACAGGTGCAAGC 2443
2161 GGCTCGGTGGGAATGGATTCCTCAAGTACCGTGGCTCTCACAAAGGACAGGTGCAAGC 2220
2444 TCATCTGCCAAGCCAAAGGCAATGGCTACTTCTGTTTGGAGCCCAAGTTGTAGATG 2503
2221 TCATCTGCCAAGCCAAAGGCAATGGCTACTTCTGTTTGGAGCCCAAGTTGTAGATG 2280
2504 GTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGAGCTG 2563
2281 GTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGAGCTG 2340
2564 GTTGTGATCGCATCATAGACTCAAAAGAAAGTTTGATTAATGTGTGTTTGGCGGGGAA 2623
2341 GTTGTGATCGCATCATAGACTCAAAAGAAAGTTTGATTAATGTGTGTTTGGCGGGGAA 2400
2624 ATGGATCTACTGTAAAGAAATATCAGGATCAGTTACTAGTGCAGAACCTGGATATCATG 2683
2401 ATGGATCTACTGTAAAGAAATATCAGGATCAGTTACTAGTGCAGAACCTGGATATCATG 2460
2684 ATATCATCAAACTTCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAACAGAGGG 2743
2461 ATATCATCAAACTTCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAAACAGAGGG 2520
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2521 GATCCAGGAACAATGGCAGCTTTCTTGCCATCAAAAGCTGTGATGGCACAATATATCTTA 2580
2804 ATGGTGAATACATCTTGTCCACTTAGCAGCAACATATGTACAAAGGTGTTGCTTGA 2863
2581 ATGGTGAATACATCTTGTCCACTTAGCAGCAACATATGTACAAAGGTGTTGCTTGA 2640
2864 GGTACAGCGCTCTCTCGCGCATTTGGAAGAAATTCGACCTTTAGCCCTCTCAAAAGAGC 2923
2641 GGTACAGCGCTCTCTCGCGCATTTGGAAGAAATTCGACCTTTAGCCCTCTCAAGAGC 2700
2924 CCTTGACCAATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATACACCT 2983
2701 CCTTGACCAATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATACACCT 2760
2984 ACTTGTAAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 3043
2761 ACTTGTAAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 2820

3044 TTGAAGAGTGGGGCGAATGTTCTTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAG 3103
2821 TTGAAGAGTGGGGCGAATGTTCTTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAG 2880
3104 AATGCCGAGACATTAATGACAGACCTGCTTCGAGTGTCAAAGGAAGTGAAGCCAGCCCA 3163
2881 AATGCCGAGACATTAATGACAGACCTGCTTCGAGTGTCAAAGGAAGTGAAGCCAGCCCA 2940
3164 GCACAGACCTTGTGTGCAGACCAATCCCTGCCAGTGGGAGTGGTCAATCAT 3223
2941 GCACAGACCTTGTGTGCAGACCAATCCCTGCCAGTGGGAGTGGTCAATCAT 3000
3224 GTTCTAAGACCTGTGGGAGGGTTACAAAAAACAAGCTTGAAGTCTGTGCTCCCATGATG 3283
3001 GTTCTAAGACCTGTGGGAGGGTTACAAAAAACAAGCTTGAAGTCTGTGCTCCCATGATG 3060
3284 GAGGGGTGTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCATAGACT 3343
3061 GAGGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCATAGACT 3120
3344 TTTGCACAATGGCAGAAATCGATTAAAGTGGTGTAAAGTGGTGTAGCTTTGAGGGCAAGGC 3403
3121 TTTGCACAATGGCAGAAATCGATTAAAGTGGTGTAAAGTGGTGTAGCTTTGAGGGCAAGGC 3180
3404 AAAGTGAAGAGGGCTGGTGCAGGGAACCAAGAGCTGGAGGGATCCAGCGTATCTTC 3463
3181 AAAGTGAAGAGGGCTGGTGCAGGGAACCAAGAGCTGGAGGGATCCAGCGTATCTTC 3240
3464 CCAGTAAACAGTGAAGTGTATCAGTAAAGTGGGATTAAGTGGGTAGATAGAAAAGGAGTT 3523
3241 CCAGTAAACAGTGAAGTGTATCAGTAAAGTGGGATTAAGTGGGTAGATAGAAAAGGAGTT 3300
3524 GAATCATCAGAGTAACACTGCCAGTTGCCAATTTGATAGGATAGTTAGTGAGGATTTATAA 3583
3301 GAATCATCAGAGTAACACTGCCAGTTGCCAATTTGATAGGATAGTTAGTGAGGATTTATAA 3360
3584 CCTCTGAGCAGTGAATAGCATTAATAAGCCCGCGGCATTTATTATTATTTCTTTTGT 3643
3361 CCTCTGAGCAGTGAATAGCATTAATAAGCCCGCGGCATTTATTATTATTATTTCTTTTGT 3420
3644 TACATCTACTACAAAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTAC 3703
3421 TACATCTATTACAAAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTAC 3480
3704 AACCCCTG 3711
3481 AACCCCTG 3488

RESULT 8

US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.560S11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308

Query Match 64.0%; Score 2570; DB 17; Length 4459; Best Local Similarity 99.5%; Pred. No. 0; Matches 3470; Conservative 0; Mismatches 18; Indels 0; Gaps 0;									
QY	224	CTCTCAGTGTCTC	CGA	CTTTGGCGTGG	AGAGAAAA	CTTCCCGCGCGCGAGAACTGCA	283		
DB	1	CTCTCAGTGTCTC	CGA	CTTTGGCGTGG	AGAGAAAA	CTTCCCGCGCGCGAGAACTGCA	60		
QY	284	GGCGCTCTCTT	AGT	CTCGGGAGCTT	CGGCTGTAG	CGGCTCTGCGCGCCCTTCCAA	343		
DB	61	GGCGCTCTCTT	AGT	CTCGGGAGCTT	CGGCTGTAG	CGGCTCTGCGCGCCCTTCCAA	120		
QY	344	CGAATAATAGAA	ATTTGTTAA	CTTAACTAT	CAAGCAGAGC	CGCAACGAGGCTTTGCTCTCC	403		
DB	121	CGAATAATAGAA	ATTTGTTAA	CTTAACTAT	CAAGCAGAGC	CGCAACGAGGCTTTGCTCTCC	180		
QY	404	CGACCCGAAT	CTAAAGTCT	CGCTCGCTCG	GTGCGCTGTAG	CGGCTCTGCGCGCCCTTCCAA	463		
DB	181	CGACCCGAAT	CTAAAGTCT	CGCTCGCTCG	GTGCGCTGTAG	CGGCTCTGCGCGCCCTTCCAA	240		
QY	464	CAATGACGAGCT	GTGCGCGAGG	GGTTCGGAAG	CGGCAAGCTT	GGCGAGCATGGGGA	523		
DB	241	CAATGACGAGCT	GTGCGCGAGG	GGTTCGGAAG	CGGCAAGCTT	GGCGAGCATGGGGA	300		
QY	524	ACGCGAGCGGCT	CTCGGGGTCT	CGAGCTTT	GGGCGGTAC	CCACGCTGTGCTGCTCG	583		
DB	301	ACGCGAGCGGCT	CTCGGGGTCT	CGAGCTTT	GGGCGGTAC	CCACGCTGTGCTGCTCG	360		
QY	584	CGCGGGGCTA	CTGGCGGTGT	CGAGC	ACTCGGGGCGCCCTT	CGAGAGGACGAGGAGC	643		
DB	361	CGCGGGGCTA	CTGGCGGTGT	CGAGC	ACTCGGGGCGCCCTT	CGAGAGGACGAGGAGC	420		
QY	644	TAGTGTGCGG	AGCTGGAGCG	CGCTCCGGG	ACACGGGAC	CGGCGCTTCCGCTGACG	703		
DB	421	TAGTGTGCGG	AGCTGGAGCG	CGCTCCGGG	ACACGGGAC	CGGCGCTTCCGCTGACG	480		
QY	704	CTTTTGAC	CAGAGCTG	GAATCTG	AGCTCGCGCGG	CAGAGCTTTTGGCGCGCGCT	763		
DB	481	CTTTTGAC	CAGAGCTG	GAATCTG	AGCTCGCGCGG	CAGAGCTTTTGGCGCGCGCT	540		
QY	764	TCAGGTCCAG	AACTGGGGCG	CAATTCGGGT	TCGAC	ACCCCGCTTCCGGAACCGGAC	823		
DB	541	TCAGGTCCAG	AACTGGGGCG	CAATTCGGGT	TCGAC	ACCCCGCTTCCGGAACCGGAC	600		
QY	824	TGGCGCACT	GTCTTACT	CCCGCAC	CGTGAATGGG	GATCCAGCTCGGCTCGCGCCCTCA	883		
DB	601	TGGCGCACT	GTCTTACT	CCCGCAC	CGTGAATGGG	GATCCAGCTCGGCTCGCGCCCTCA	660		
QY	884	GCCTCTG	CGAGGCGT	GTGCGCGCTT	CTACTGT	GTGGGAGGCGTATTTTCACTCCAGC	943		
DB	661	GCCTCTG	CGAGGCGT	GTGCGCGCTT	CTACTGT	GTGGGAGGCGTATTTTCACTCCAGC	720		
QY	944	CGCTGCGCG	CGCAGCGCT	GTGCGCAC	CGCGCGCCCG	CAGGGAGAGCGCGCGGAC	1003		
DB	721	CGCTGCGCG	CGCAGCGCT	GTGCGCAC	CGCGCGCCCG	CAGGGAGAGCGCGCGGAC	780		
QY	1004	CACCTAC	AGTTCCACT	CTCTGCGCGG	AAATCGGCGG	CGACCTAGCGCGACGTCGGGG	1063		
DB	781	CACCTAC	AGTTCCACT	CTCTGCGCGG	AAATCGGCGG	CGACCTAGCGCGACGTCGGGG	840		
QY	1064	TCGTGGA	CGACGAGCG	CGCGCGCT	GTGGGAAAG	CGGAGACCGAAGACGAGGGA	1123		
DB	841	TCGTGGA	CGACGAGCG	CGCGCGCT	GTGGGAAAG	CGGAGACCGAAGACGAGGGA	900		
QY	1124	CTGAGGCG	GAGGAGCG	AGGCGCT	CTAGTGT	CGCGCGGAGGACCGCGGCTAG	1183		
DB	901	CTGAGGCG	GAGGAGCG	AGGCGCT	CTAGTGT	CGCGCGGAGGACCGCGGCTAG	960		
QY	1184	GACGCGCA	GAGAACT	GGAAGCA	TAAGAAAG	CGATTTGTCAGTCAACCGCTATG	1243		
DB	961	GACGCGCA	GAGAACT	GGAAGCA	TAAGAAAG	CGATTTGTCAGTCAACCGCTATG	1020		
QY	1244	TGGAACCA	TGCTTGT	GGCAGAC	CGAGT	CGATTCGAGAGATTTCCACGGCGAGTGGTCTAAAGC	1303		


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Db 2101 CCTTTAGAGAGAAACAATGTGAAGCACACACAGAGTTTTTCAAAAGCTTCCTTTGGAGTG 2160
Qy 2384 GGCCTGCGGTGGAATGGATTTCCCAAGTACGCTGGGCTCTCACAAAGGACAGGTGCAAGC 2443
Db 2161 |||||
Qy 2444 TCATCTGCCAAGCCAAAGGCATTTGGCTACTTCTCGTTTTTGACGCCAACAGGTGTAGATG 2503
Db 2221 TCATCTGCCAAGCCAAAGGCATTTGGCTACTTCTCGTTTTTGACGCCAACAGGTGTAGATG 2280
Qy 2504 GTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGACAGTGTGTAAAGCTG 2563
Db 2281 GTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGACAGTGTGTAAAGCTG 2340
Qy 2564 GTTGTGATCGCATCATAGACTCCAAAAGAGAGTTTGCATAAATGTGTGTTTTGCGGGGAA 2623
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Qy 2804 ATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGA 2863
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Qy 2864 GGTACAGCGGCTCCTCTGCGGCATTTGGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGC 2923
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Qy 2984 ACTTCGTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 3043
Db 2761 ACTTCGTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 2820
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Qy 3104 AATGCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAGAGGAGTGAAGCCAGCCA 3163
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Qy 3284 GAGGGTGTATCTCATGACAGCTGTGATCTTTTAAAGAACCTTAAACATTTTCATAGACT 3343
Db 3061 GAGGGTGTATCTCATGACAGCTGTGATCTTTTAAAGAACCTTAAACATTTTCATAGACT 3120
Qy 3344 TTTTGCAATGTGGCAGATTCAGTGAAGTGTGTTAAGTGTGTGTAGCTTTGAGGCGAAGGC 3403
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Db 3181 AAAGTGAAGGAGGGCTGTGTGAGGGAAGCAAGAGGCTGGAGGATTCAGCGGTATCTTC 3240
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Qy 3464 CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTATGGGGGTAGATAGAAAAAGAGTT 3523
Db 3241 CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTATGGGGGTAGATAGAAAAAGAGTT 3300
Qy 3524 GAATCATCAGAGTAACCTGCCAGTTTGCAAATTTGATAGGATAGTTAGTGAGGATTTATAA 3583
Db 3301 GAATCATCAGAGTAACCTGCCAGTTTGCAAATTTGATAGGATAGTTAGTGAGGATTTATAA 3360
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Qy 3644 TACATCTACTACAGTTTAAAAAACAAGCAATTTGTCAAAAAAGTTAGAACCTATTAC 3703
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Qy 3704 AACCCCTG 3711
Db 3481 AACCCCTG 3488

RESULT 9
US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US2004026580A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN, ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Query Match 63.5%; Score 2548; DB 18; Length 3430;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3318; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Qy 280 TGAGCGGCTCTCTTTAGTGACTCCCGGAGCTTCGGCTGTAGCGGCTCTGCGGCGCTT 339
Db 1 TGAGCGGCTCTCTTTAGTGACTCCCGGAGCTTCGGCTGTAGCGGCTCTGCGGCGCTT 60
Qy 340 CGAACCAATTAAGAAATTTAAATTTTAAATCCAGACAGCCAAACGAGGCTTTGCT 399
Db 61 CCAACCAATTAAGAAATTTAAATTTTAAATCCAGACAGCCAAACGAGGCTTTGCT 120
Qy 400 CTCGCCACCGCAACTAAAGCTCCCTCGCTCGCTGCTGTACGAGCGGTGTCTCTCGGG 459
Db 121 CTCGCCACCGCAACTAAAGCTCCCTCGCTCGCTGCTGTACGAGCGGTGTCTCTCGGG 180
Qy 460 GCTTCCAATGCAGCAGCTGTGTGCCGAGGGTTCCGAAGGCGCAAGCTGGGCGAGCATG 519
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181	Db		GCTCCAATG	CAGCAGCTGTGCCCGAGGGGTTCGGAAGGCGCAGCTGGCGACGCAATG	240
520	Qy	GGGAACGCGAG	CGGGGTCTCGAGCTTTTCGGGCCGCTACCCACGCTGCTGCTG	579	
241	Db	GGGAACGCGAG	CGGGGTCTCGAGCTTTTCGGGCCGCTACCCACGCTGCTGCTG	300	
580	Qy	CTCGCCCGCGCT	TACTGGCCGTCTCGGAAGCACTCGGGGGCCCTCCGAGGAGGACGAG	639	
301	Db	CTCGCCCGCGCT	TACTGGCCGTCTCGGAAGCACTCGGGGCCCTCCGAGGAGGACGAG	360	
640	Qy	GAGCTAGTGTG	TCGGAAGCTTCCCGGAACAACGCGACCAACGCGCTTCCGCGCTG	699	
361	Db	GAGCTAGTGTG	TCGGAAGCTTCCCGGAACAACGCGACCAACGCGCTTCCGCGCTG	420	
700	Qy	CAGCGCTTTGAC	CAGCAGCTGGATCTCGAGCGTGC CGCCCGACACGACGACTTTTGGCGCCC	759	
421	Db	CAGCGCTTTGAC	CCAGCAGCTGGATCTCGAGCTGGCGCCCGACACGACGACTTTTGGCGCCC	480	
760	Qy	GGCTTTCACGCT	TCAGAAACGTGGGCGCAAAATCTCGGGTCCGACACCCCGCTTCCGGAAC	819	
481	Db	GGCTTTCACGCT	TCAGAAACGTGGGCGCAAAATCTCGGGTCCGAGACCGCTTCCGGAAC	540	
820	Qy	GACTGTGGCACT	GTCTTACTCCGGCAACCGTGAATGGCGATCCAGCTCGGTGCGCGCC	879	
541	Db	GACTGTGGCACT	GTCTTACTCCGGCAACCGTGAATGGCGATCCAGCTCGGTGCGCGCC	600	
880	Qy	CTCAGCCTCTG	CGAGGGCGTGGCGCGCTTCTACCTGCTGGGGAGGCGTATTTCATC	939	
601	Db	CTCAGCCTCTG	CGAGGGCGTGGCGCGCTTCTACCTGCTGGGGAGGCGTATTTCATC	660	
940	Qy	CAGCGCTGCGC	CGCGCAGCAGCGCTCGCCACCGCCCGCCAGGGGAGAGCCGCG	999	
661	Db	CAGCGCTGCGC	CGCGCAGCAGCGCTCGCCACCGCCCGCCAGGGGAGAGCCGCG	720	
1000	Qy	GCACCACTACAG	TTCCAACCTCTGCGCGGGAATCGGCAGGCGCACTGAGCGCGCACTGC	1059	
721	Db	GCACCACTACAG	TTCCAACCTCTGCGCGGGAATCGGCAGGCGCACTGAGCGCGCACTGC	780	
1060	Qy	GGGCTGTGAC	ACGACGACCCCGCCGACCTGGGGAACGGGAGACCGGAACGAGGACGAA	1119	
781	Db	GGGCTGTGGA	CGACGACCCCGCCGACCTGGGGAACGGGAGACCGGAACGAGGACGAA	840	
1120	Qy	GGGACTCAGGG	CGAGGAGCGCTCAGTGTGTCGCGCAGGACCGGCACTGCAAGGC	1179	
841	Db	GGGACTCAGGG	CGAGGAGCGCTCAGTGTGTCGCGCAGGACCGGCACTGCAAGGC	900	
1180	Qy	GTAGGACAGCC	CAACAGGAACTGGAAGCATGAAGAAAGCGATTTGTGTCAGTCAACCGC	1239	
901	Db	GTAGGACAGCC	CAACAGGAACTGGAAGCATGAAGAAAGCGATTTGTGTCAGTCAACCGC	960	
1240	Qy	TATGTGAAAC	CAATGCTTGTGGCAGACCGTGCATGTCAGAAATCCACGGCAGTGTCTA	1299	
961	Db	TATGTGAAAC	CAATGCTTGTGGCAGACCGTGCATGTCAGAAATCCACGGCAGTGTCTA	1020	
1300	Qy	AAGCATTTAC	CTTCTCAGCTTGTGTTTTCGTGGCGACCGATTTGTATACAAACCCCGCAT	1359	
1021	Db	AAGCATTTAC	CTTCTCAGCTTGTGTTTTCGTGGCGACCGATTTGTATACAAACCCCGCAT	1080	
1360	Qy	CGTAATTT	CAGTTAGCTGCTGGTGGTGAAGATCTTGTGTCATCCACGATGAACGAGGGG	1419	
1081	Db	CGTAATTT	CAGTTAGCTGCTGGTGGTGAAGATCTTGTGTCATCCACGATGAACGAGGGG	1140	
1420	Qy	CCCGAAGTG	ACCTCAATGCTGCCCTCACTCTGCGGAACTTTTGCACTGGCAGAGCAG	1479	
1141	Db	CCCGAAGTG	ACCTCAATGCTGCCCTCACTCTGCGGAACTTTTGCACTGGCAGAGCAG	1200	
1480	Qy	CACAACCC	ACCCAGTGACCGGATGACAGCACTATCACACAGCAATCTCTTTTACCAGA	1539	
1201	Db	CACAACCC	ACCCAGTGACCGGATGACAGCACTATCACACAGCAATCTCTTTTACCAGA	1260	
1540	Qy	CAGGACTTGT	TGGGTCCGACATGTGATCTCTTGGGATGGCTGATTTGGAACTGTG	1599	

[illegible]

QY 2680 CATGATATCATCAATTCACATTCGAGCCACCAACATCGAGTGAACAGCGGAAACCCAG 2739
DB 2401 CATGATATCATCAATTCACATTCGAGCCACCAACATCGAGTGAACAGCGGAAACCCAG 2460
QY 2740 AGGGATCCAGGAAACAAATGGCAGCTTTCTTGCCATCAAGAGCTGCTGATGCGACATATTT 2799
DB 2461 AGGGATCCAGGAAACAAATGGCAGCTTTCTTGCCATCAAGAGCTGCTGATGCGACATATTT 2520
QY 2800 CTTAATGGTGACTACACTTTGTCCACTTAGACGAGACATTAATGACAAAGTGTGTC 2859
DB 2521 CTTAATGGTGACTACACTTTGTCCACTTAGACGAGACATTAATGACAAAGTGTGTC 2580
QY 2860 TTGAGGTACAGCGGCTCTCTGCGGCAATTCGAAAGAAATTCGAGCTTTAGCCCTCTCAAA 2919
DB 2581 TTGAGGTACAGCGGCTCTCTGCGGCAATTCGAAAGAAATTCGAGCTTTAGCCCTCTCAAA 2640
QY 2920 GAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATTCGAGCTTTAGCCCTCTCAAAATTAATAC 2979
DB 2641 GAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATTCGAGCTTTAGCCCTCTCAAAATTAATAC 2700
QY 2980 ACTTACTTGTAAAGAAAGAAAGAAATCTTCAATGCTATCCCACTTTTTCAGCATGG 3039
DB 2701 ACTTACTTGTAAAGAAAGAAAGAAATCTTCAATGCTATCCCACTTTTTCAGCATGG 2760
QY 3040 GTCATTTGAAGAGTGGGCGGAATGTTCTAAGTCAATGTAATTTGGTGGCAGAGAACTG 3099
DB 2761 GTCATTTGAAGAGTGGGCGGAATGTTCTAAGTCAATGTAATTTGGTGGCAGAGAACTG 2820
QY 3100 GTAGAATGCCGAGACATTAATGACAGCTGCTTCCAGAGTGTGCAAGAAAGTGAAGCCA 3159
DB 2821 GTAGAATGCCGAGACATTAATGACAGCTGCTTCCAGAGTGTGCAAGAAAGTGAAGCCA 2880
QY 3160 GCAGACACAGACTTTGTGAGACCATCTCTGCCCCCAGCTGGCAGCTGGGGGAGTGTCA 3219
DB 2881 GCAGACACAGACTTTGTGAGACCATCTCTGCCCCCAGCTGGCAGCTGGGGGAGTGTCA 2940
QY 3220 TCATGTTCTAAGACCTGTGGGAGGGTTTACAAAAGAAAGCTTGAAGTGTCTGTGCCAT 3279
DB 2941 TCATGTTCTAAGACCTGTGGGAGGGTTTACAAAAGAAAGCTTGAAGTGTCTGTGCCAT 3000
QY 3280 GATGGAGGGTGTATCTCATGACAGCTGTGATCTTTAAAGAAACCTTAAACATTTTCA 3339
DB 3001 GATGGAGGGTGTATCTCATGACAGCTGTGATCTTTAAAGAAACCTTAAACATTTTCA 3060
QY 3340 GACTTTTGCACAATGGCAGAAATGCAAGTTAAGTGGTTAAGTGTGTAGCTTTGAGGGCA 3399
DB 3061 GACTTTTGCACAATGGCAGAAATGCAAGTTAAGTGGTTAAGTGTGTAGCTTTGAGGGCA 3119
QY 3400 AGGCAAGTGCAGGAAGGGCTGTGCAAGGAAAGCAAGAGGCTGGAGGGATCCAGGCTAT 3459
DB 3120 AGGCAAGTGCAGGAAGGGCTGTGCAAGGAAAGCAAGAGGCTGGAGGGATCCAGGCTAT 3179
QY 3460 CTTTCCAGTAACAGAGTGTATCAAGTAAAGTGGGATTTATGGGGGTAGATAGAAAGG 3519
DB 3180 CTTTCCAGTAACAGAGTGTATCAAGTAAAGTGGGATTTATGGGGGTAGATAGAAAGG 3239
QY 3520 AGTTGAATCATCAGATTAACCTGCGAGTTGCAATTTGATAGATAGATAGATAGATTA 3579
DB 3240 AGTTGAATCATCAGATTAACCTGCGAGTTGCAATTTGATAGATAGATAGATAGATTA 3299
QY 3580 TTAACCTCTGAGCAGTGTATAGCATTAATAA 3611
DB 3300 TTAACCTCTGAGCAGTGTATAGCATTAATAA 3331

RESULT 10

US-10-667-281-1

; Sequence 1, Application US/10667281
; Publication No. US20050100916A1
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John

; APPLICANT: Heller, Remu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/10/667,281
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
; US-10-667-281-1

Query Match 61.6%; Score 2471; DB 19; Length 3889;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 476 CTGTGCCCCGAGGGGTTTCGGAAGCGCAAGCTGGGCGACGACATGGGGAACCGCGAGCGGG 535
DB 18 CTGTGCCCCGAGGGGTTTCGGAAGCGCAAGCTGGGCGACGACATGGGGAACCGCGAGCGGG 77
QY 536 CTCGGGGTCTCGGAGCTTTGGGCGGTACCCACGCTGCTGCTGCTGCGCGCGCGCTAC 595
DB 78 CTCGGGGTCTCGGAGCTTTGGGCGGTACCCACGCTGCTGCTGCTGCGCGCGCGCTAC 137
QY 596 TGGCCCTGTGCGAGCGCACTCGGGCGGCCCTCCGAGGAGGACGAGGAGCTAGTGTGTCGG 655
DB 138 TGGCCCTGTGCGAGCGCACTCGGGCGGCCCTCCGAGGAGGACGAGGAGCTAGTGTGTCGG 197
QY 656 AGCTGAGCGCGTTCGCGGACACGCGGACCAACGCGCTTCGCGCTTGCAGCCTTTGACGAGC 715
DB 198 AGCTGAGCGCGTTCGCGGACACGCGGACCAACGCGCTTCGCGCTTGCAGCCTTTGACGAGC 257
QY 716 AGCTGAGCTGGAAGTGGCGCGCGCGAGCAGGAGCTTTTGGCGCGCGCTTCCAGCTCCAGA 775
DB 258 AGCTGAGCTGGAAGTGGCGCGCGCGAGCAGGAGCTTTTGGCGCGCGCTTCCAGCTCCAGA 317
QY 776 ACCTGGGGCGGCAATCCGGTCCGACACACCCCGCTTCGGAACCGAGCTGCGCGCACTGCT 835
DB 318 ACCTGGGGCGGCAATCCGGTCCGAGCGCGCTTCGGAACCGAGCTGCGCGCACTGCT 377
QY 836 TCTACTCCGGCACCGTGAATGCGGATCCGAGCTCGGCTGCGCGCTTGCAGCCTTCTGCGAGG 895
DB 378 TCTACTCCGGCACCGTGAATGCGGATCCGAGCTCGGCTGCGCGCTTGCAGCCTTCTGCGAGG 437
QY 896 GCGTGGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCGCTGCGCGCGCG 955
DB 438 GCGTGGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCGCTGCGCGCGCG 497
QY 956 CCAGCAGCGCTTCGCGACCGCGCGCGCGCGAGGAGCGCGCGCGCACCACTACAGTTCC 1015
DB 498 CCAGCAGCGCTTCGCGACCGCGCGCGCGCGAGGAGCGCGCGCACCACTACAGTTCC 557
QY 1016 ACCTCTCGCGCGGCAATTCGCGAGCGGCGAGCTAGCGGCGACGCTGCGGGGTCTGTGAGCAGC 1075
DB 558 ACCTCTCGCGCGGCAATTCGCGAGCGGCGAGCTAGCGGCGACGCTGCGGGGTCTGTGAGCAGC 617
QY 1076 AGCCCGCGCGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGAGGGCGCGAGG 1135
DB 618 AGCCCGCGCGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGAGGGCGCGAGG 677
QY 1136 ACGAAGGGCTCTAGTGTGCTGCCCGCAGGACCCCGCAGCTGCAAGGCTAGGAGCAGCCACAG 1195
DB 678 ACGAAGGGCTCTAGTGTGCTGCCCGCAGGAGCCCGCAGCTGCAAGGCTAGGAGCAGCCACAG 737
QY 1196 GAATCGAAGCATTAAGAAAGAGCGATTTGTGTCCAGTCAACCGCTATGTGTGAACCAATGC 1255

Db 738 GAACTGGAAGCATAGAAGAGCGATTGTTGTCACAGTCCACCGCTATTGTGGAACCATGCG 797
QY 1256 TTGTGGCAGACAGTCGATGGCAGAAATCCACGGCAGTGGTCTAAAGCATTTACCTTCTCA 1315
Db 798 TTGTGGCAGACAGTCGATGGCAGAAATCCACGGCAGTGGTCTAAAGCATTTACCTTCTCA 857
QY 1316 CQTGTGTTTTCGGTGGCAGCAGATTGTACAAACACCCACAGCATTCGTAAATCAGTTAGCC 1375
Db 858 CQTGTGTTTTCGGTGGCAGCAGATTGTACAAACACCCACAGCATTCGTAAATCAGTTAGCC 917
QY 1376 TGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAGGGGGCCGAGTGACCTCCA 1435
Db 918 TGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAGGGGGCCGAGTGACCTCCA 977
QY 1436 ATGCTGCCCTCACTCTGGGAACTTTGCAACTGSCAGNAGCAGCAACACCACCGAGTG 1495
Db 978 ATGCTGCCCTCACTCTGGGAACTTTGCAACTGSCAGNAGCAGCAACACCACCGAGTG 1037
QY 1496 ACCGGGATGCAGACACTATGACACAGCAATTTCTTTTACCACAGACGAGCTTGTGTGGGT 1555
Db 1038 ACCGGGATGCAGACACTATGACACAGCAATTTCTTTTACCACAGACGAGCTTGTGTGGGT 1097
QY 1556 CCACAGCATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAA 1615
Db 1098 CCACAGCATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAA 1157
QY 1616 GCTGCTCGTCTAGAGATGATGTTTACAGCTGCTTACACAGCCCATGAAATAG 1675
Db 1158 GCTGCTCGTCTAGAGATGATGTTTACAGCTGCTTACACAGCCCATGAAATAG 1217
QY 1676 GCCAGTGTAAACATGCCACATGATGACAAAGCAGTGCACAGCTTAAATGTGTGA 1735
Db 1218 GCCAGTGTAAACATGCCACATGATGACAAAGCAGTGCACAGCTTAAATGTGTGA 1277
QY 1736 ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTCGACACACAGCCCTTGGT 1795
Db 1278 ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTCGACACACAGCCCTTGGT 1337
QY 1796 CTCCTTGAGTGGCTACATGATTACATCATTTCTGGATTAAGTCAATGGGAAATGTTGA 1855
Db 1338 CTCCTTGAGTGGCTACATGATTACATCATTTCTGGATTAAGTCAATGGGAAATGTTGA 1397
QY 1856 TGGACAAGCTCCAGAAATCCATACAGCTCCACAGGCGATCTCCCTGCGACCTCGTACGATG 1915
Db 1398 TGGACAAGCTCCAGAAATCCATACAGCTCCACAGGCGATCTCCCTGCGACCTCGTACGATG 1457
QY 1916 CCAACCGGCAGTGCACGATTTACATTTGGGGAGGACTCCAAACACTGCCCTGATGACGCA 1975
Db 1458 CCAACCGGCAGTGCACGATTTACATTTGGGGAGGACTCCAAACACTGCCCTGATGACGCA 1517
QY 1976 GCACATGTAGCACTTGTGGTGTACGGGACCTCTGTTGGGGTGTGTTGTCTCAACCA 2035
Db 1518 GCACATGTAGCACTTGTGGTGTACGGGACCTCTGTTGGGGTGTGTTGTCTCAACCA 1577
QY 2036 AACACTTCCGTTGGCGGATGACACAGCTGTGGAGAGGAAATGTTGTATCAACGGCA 2095
Db 1578 AACACTTCCGTTGGCGGATGACACAGCTGTGGAGAGGAAATGTTGTATCAACGGCA 1637
QY 2096 AGTGTGTGAACAAAAACCAAGAAAGCAATTTGATACGCTTTTTCATGGAAGCTGGGAA 2155
Db 1638 AGTGTGTGAACAAAAACCAAGAAAGCAATTTGATACGCTTTTTCATGGAAGCTGGGAA 1697
QY 2156 TGTGGGGGCTTTGGGAGACTGTTTCAGAGAACCTGTCGGTGGAGAGTCCAGTACAGATGA 2215
Db 1698 TGTGGGGGCTTTGGGAGACTGTTTCAGAGAACCTGTCGGTGGAGAGTCCAGTACAGATGA 1757
QY 2216 GCGAATGTCAACACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGCCAAACAGATGC 2275
Db 1758 GCGAATGTCAACACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGCCAAACAGATGC 1817
QY 2276 GCTACAGATCTGTAACTTTGAGGACTGTCCAGACAAATTAATGGAAAAACCTTTAGAGAG 2335
Db 1818 GCTACAGATCTGTAACTTTGAGGACTGTCCAGACAAATTAATGGAAAAACCTTTAGAGAG 1877

QY 2336 AACATGTGAAGCACACAAACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGCTCGGTGG 2395
Db 1878 AACATGTGAAGCACACAAACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGCTCGGTGG 1937
QY 2396 AATGGATTTCCCAAGTACGCTGGCGTCTCACAAAGGACAGGTGCAAGCTCATCTGCCAAG 2455
Db 1938 AATGGATTTCCCAAGTACGCTGGCGTCTCACAAAGGACAGGTGCAAGCTCATCTGCCAAG 1997
QY 2456 CCAAGGCAATTTGGCTACCTTCTTGGTTTTCGACCCCAAGTTGTAGATGGTACTCATGTA 2515
Db 1998 CCAAGGCAATTTGGCTACTTCTTGGTTTTCGACCCCAAGTTGTAGATGGTACTCATGTA 2057
QY 2516 GCCCAGATTTCCACCTCTCTGTGTGCAAGACAGTGTAAAGCTGTTGTGTGATCGCA 2575
Db 2058 GCCCAGATTTCCACCTCTCTGTGTGCAAGACAGTGTGTAAAGCTGTTGTGTGATCGCA 2117
QY 2576 TCATAGACTCCAAAAGAAAGTTTGTATAAATGTGGTGTGTTTGGGGGAAATGATCTACTT 2635
Db 2118 TCATAGACTCCAAAAGAAAGTTTGTATAAATGTGGTGTGTTTGGGGGAAATGATCTACTT 2177
QY 2636 GTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAAA 2695
Db 2178 GTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAAA 2237
QY 2696 TTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAAACAGAGGGATCCAGAAACA 2755
Db 2238 TTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAAACAGAGGGATCCAGAAACA 2297
QY 2756 ATGGCAGCTTTCTTGGCCATCAAAAGCTGTGATGGCACATATATCTTAAATGGTGACTACA 2815
Db 2298 ATGGCAGCTTTCTTGGCCATCAAAAGCTGTGATGGCACATATATCTTAAATGGTGACTACA 2357
QY 2816 CTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGTGTGTTCTTGTAGAGTACACGGCT 2875
Db 2358 CTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGTGTGTTCTTGTAGAGTACACGGCT 2417
QY 2876 CCTCTGGCGCATGGAGAGAAATTCGACGCTTTAGCCCTCTCAAAAGAGCCCTTGACATCC 2935
Db 2418 CCTCTGGCGCATGGAGAGAAATTCGACGCTTTAGCCCTCTCAAAAGAGCCCTTGACATCC 2477
QY 2936 AGTGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAACCTACTCTCGTAAAGA 2995
Db 2478 AGTGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAACCTACTCTCGTAAAGA 2537
QY 2996 AGAAGAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAATGAGAGTGGG 3055
Db 2538 AGAAGAGAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAATGAGAGTGGG 2597
QY 3056 GCGAATGTTCTAAGTCATGTGAATTTGGGTTTGGCAGAGAACTGTTAGAAATGCCGAGACA 3115
Db 2598 GCGAATGTTCTAAGTCATGTGAATTTGGGTTTGGCAGAGAACTGTTAGAAATGCCGAGACA 2657
QY 3116 TTAATGAGCAGCTGTCTTTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGCAGACCTTT 3175
Db 2658 TTAATGAGCAGCTGTCTTTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGCAGACCTTT 2717
QY 3176 GTGAGACATCTCTGCCCCAGTGCGGAGTGGGGAGTGTGTCATCATGTTCTTAAGACT 3235
Db 2718 GTGAGACATCTCTGCCCCAGTGCGGAGTGGGGAGTGTGTCATCATGTTCTTAAGACT 2777
QY 3236 GTGGGAAGGGTTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTAT 3295
Db 2778 GTGGGAAGGGTTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTAT 2837
QY 3296 CTCATGACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTCTATAGACTTTTGCAAAATGG 3355
Db 2838 CTCATGACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTCTATAGACTTTTGCAAAATGG 2897
QY 3356 CAGAATGACAGTTAAGTGTGTTAAGTGGTGTAGCTTTTGGGGCAAGGCAAGGTGAGGAG 3415
Db 2898 CAGAATGACAGTTAAGTGTGTTAAGTGGTGTAGCTTTTGGGGCAAGGCAAGGTGAGGAG 2957

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QY 3416 GGCTGGTGCAGGAAAGCAAGAGGCTGAGGAGTCCAGCGTATCTTCCAGTAACAGT 3475
Db 2958 GGCTGGTGCAGGAAAGCAAGAGGCTGAGGAGTCCAGCGTATCTTCCAGTAACAGT 3017
QY 3476 GAGGTGTATCAGTAAGTGGATATATGCGGGTATAGTAAAGAGGATTTGAATCATCAGAG 3535
Db 3018 GAGGTGTATCAGTAAGTGGATATATGCGGGTATAGTAAAGAGGATTTGAATCATCAGAG 3077
QY 3536 TAAACTGCCAGTTTGCAAAATTTGATAGATAGTATAGTGAAGATATTAAACCTCTGAGCAGT 3595
Db 3078 TAAACTGCCAGTTTGCAAAATTTGATAGATAGTATAGTGAAGATATTAAACCTCTGAGCAGT 3137
QY 3596 GATATAGCATATAAAGCCCGGCGCATTTATTTATTTATTTCTTTTGTATCATCTACTAC 3655
Db 3138 GATATAGCATATAAAGCCCGGCGCATTTATTTATTTATTTCTTTTGTATCATCTATTAC 3197
QY 3656 AGTTTAAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTATTACAAACCCCTG 3711
Db 3198 AGTTTAAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTATTACAAACCCCTG 3253

RESULT 11
US-10-741-600-776
; Sequence 776, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 4352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4352)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-776

Query Match 61.4%; Score 2463; DB 19; Length 4352;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3763; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 25 GCGGCTCCGAGCCAGGGGCTATTGCAAGCCAGGGTGGCTACCGGACGGAGAGGGGAGA 84
Db 21 GCGGCTCCGAGCCAGGGGCTATTGCAAGCCAGGGTGGCTACCGGACGGAGAGGGGAGA 80
QY 85 GCCTTAGCAGAGTAGACAAATCGCAGCCAGGCGGAGCCGGAAGAGGGGCGCAGGCA 144
Db 81 GCCTTAGCAGAGTAGACAAATCGCAGCCAGGCGGAGCCGGAAGAGGGGCGCAGGCA 140
QY 145 CCAATCTCCGGTGGCTCTCAGTGTCTCCAACTTTTGGCTGGAGAAACTTTCCC 264
Db 141 CCAATCTCCGGTGGCTCTCAGTGTCTCCAACTTTTGGCTGGAGAAACTTTCCC 260
QY 205 CCACTCTGGCTGGCTGGCTCTCAGTGTCTCCAACTTTTGGCTGGAGAAACTTTCCC 264
Db 201 CCACTCTGGCTGGCTGGCTCTCAGTGTCTCCAACTTTTGGCTGGAGAAACTTTCCC 260
QY 265 GCGGCGCGCAGAACTCAGCGGCTCTCTTAGTGAATCTCCGGGAGCTTCGGCTGTAGCGG 324
Db 261 GCGGCGCGCAGAACTCAGCGGCTCTCTTAGTGAATCTCCGGGAGCTTCGGCTGTAGCGG 320
QY 325 GCTCTGCGGCGGCTTCCAAAGTAATAGAAATTTTAACTTAACATCAGAGCAGGC 384
Db 321 GCTCTGCGGCGGCTTCCAAAGTAATAGAAATTTTAACTTAACATCAGAGCAGGC 380
QY 385 CAAGAGGGCTTGTCTCTCCGACCCGAACTAAAGCTCCCTCGCTCCGCTGCTACGA 444
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Db 381 CAACGAGGCTTGTCTCTCCGACCCGAACTTAAAGSTCCCTCGCTCGCTGCGTCTACGA 440
QY 445 GGGTGTCTCTCTGGGGCTCCAAATGACGAGCTGTCCCGAGGGGTTCGGAAGCGCGCAAG 504
Db 441 GGGTGTCTCTCTGGGGCTCCAAATGACGAGCTGTCCCGAGGGGTTCGGAAGCGCGCAAG 500
QY 505 CTGGGCGAGCAGATATGGGGAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCCCGTA 564
Db 501 CTGGGCGAGCAGATATGGGGAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCCMGTA 560
QY 565 CCACGCTGTGTCTGTCTGCGCGCGCGCTACTGCGCGTGTTCGACGCACTCTGGGCGGCC 624
Db 561 CCACGCTGTGTCTGTCTGCGCGCGCGCTACTGCGCGTGTTCGACGCACTCTGGGCGGCC 620
QY 625 TCCGAGGAGCAGAGGAGCTAGTGTGCGGAGCTGAGCGCTCCGGGACACAGGAGC 684
Db 621 TCCGAGGAGCAGAGGAGCTAGTGTGCGGAGCTGAGCGCTCCGGGACACAGGAGC 680
QY 685 ACGCGCTCCGCTGCAAGCTTTTGACAGCAGCTGATCTGAGCGTGCCTCCCGCAGCAGC 744
Db 681 ACGCGCTCCGCTGCAAGCTTTTGACAGCAGCTGATCTGAGCGTGCCTCCCGCAGCAGC 740
QY 745 AGCTTTTGGCGCGCGCTTACGCTTCAGAACTGCGGGCGCAAAATCCGGGTTCGACAC 804
Db 741 AGCTTTTGGCGCGCGCTTACGCTTCAGAACTGCGGGCGCAAAATCCGGGTTCGAGACG 800
QY 805 CGCTTTCCGGAACCCAGCTTGGCGCACTGCTTCTACTCCGGCACCGTGAATGCGATCCC 864
Db 801 CGCTTTCCGGAACCCAGCTTGGCGCACTGCTTCTACTCCGGCACCGTGAATGCGATCCC 860
QY 865 AGCTCGGCTGCGCGCTCTGAGCGGTGCGCGCGCTTCTACTCTGCTGCGG 924
Db 861 AGCTCGGCTGCGCGCTCTGAGCGGTGCGCGCGCTTCTACTCTGCTGCGG 920
QY 925 GAGCGTATTTATTCAGCGCTGCGCGCGCTGCGCGAGCGCTTCCGACCGCGGCCCA 984
Db 921 GAGCGTATTTATTCAGCGCTGCGCGCGCTGCGCGAGCGCTTCCGACCGCGGCCCA 980
QY 985 GGGAGAGCGCGCGCACCACTACAGTTCCACTCTCTGCGCGGGAATCCGGAGGGCGAC 1044
Db 981 GGGAGAGCGCGCGCGCACCACTACAGTTCCACTCTCTGCGCGGGAATCCGGAGGGCGAC 1040
QY 1045 GTAGGCGGACAGTGGGGTCTGTGAGCAGCAGCGCGCGCTGGAAGAGGAGCAGC 1104
Db 1041 GTAGGCGGACAGTGGGGTCTGTGAGCAGCAGCGCGCGCTGGAAGAGGAGCAGC 1100
QY 1105 GAAGACGAGACGAAAGGAGCTGAGGGGAGGAGCAGAGGGCTCAGTGTGCGCGCAGCAG 1164
Db 1101 GAAGACGAGACGAAAGGAGCTGAGGGGAGGAGCAGAGGGCTCAGTGTGCGCGCAGCAG 1160
QY 1165 CCGGCACTGCAAGCGCTAGGACAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATTT 1224
Db 1161 CCGGCACTGCAAGCGCTAGGACAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATTT 1220
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; GENERAL INFORMATION:						
; APPLICANT: Chinnaiyan, Arul M.						
; APPLICANT: Rubin, Mark A.						
; APPLICANT: Sreekumar, Arun						
; TITLE OF INVENTION: Expression Profile of Prostate Cancer						
; FILE REFERENCE: UM-07221						
; CURRENT APPLICATION NUMBER: US/10/210,120						
; CURRENT FILING DATE: 2002-08-01						
; PRIOR APPLICATION NUMBER: US 60/309,581						
; PRIOR FILING DATE: 2001-08-02						
; PRIOR APPLICATION NUMBER: US 60/334,468						
; PRIOR FILING DATE: 2001-11-15						
; NUMBER OF SEQ ID NOS: 123						
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; SEQ ID NO 57						
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QY	411	AACCTAAGCTCCCTCGCTCGCTGCTGCTAGAGCGGCTGCTCTCGGGCTCCAAATGCA	470	1011	GTTCCACCTCCTCGCGCGGAAATCGGCAGGCGACGTTAGCGGCACGCTGCGGGTCTGTGA	1070
DB	61	AACCTAAGCTCCCTCGCTCGCTGCTGCTAGAGCGGCTGCTCTCGGGCTCCAAATGCA	120	661	GTTCCACCTCCTCGCGCGGAAATCGGCAGGCGACGTTAGCGGCACGCTGCGGGTCTGTGA	720
QY	471	GCAGAGCTGTGCCGAGGGGTTCCGAGCGCGCAAGCTGGGCGAGCAGACATGGGGAAACCGGA	530	1071	CGACGAGCCCCCGCCGACTTGGGAAAGCGGAGACCGAAGACCGAGGACGAGGACTGAGGG	1130
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QY	531	GCGGGCTCCGGGCTTCGAGAGCTTTGGGCGCGTACCAACGCTGCTGCTCGCGCGGC	590	1131	CGAGGACGAGGCGCTCAGTGTGCGCGAGGACCGGACCTCCAGGCGTAGGACAGCC	1190
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DB	241	GCTACTGCGCGTGTGCGAGCAGCTCGGCGCGCCCTCCGAGGAGGACGAGGAGCTAGTGGT	300	841	CAAGGAACTGGAGCATTAAGAAAGCGGATTTGTTCAGTCACCGCTATGTGGAAAC	900
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QY	711	CCAGCAGCTGATCTGAGAGTGTGCGCGCGCAGCAGAGCTTTTGGCGCGCGCTTACGCT	770	1311	TCTCAGCTTGTTCGGTGGCAGCAGATTTGTACAAACACCCAGCATTCGTAATTCAGT	1370
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QY 2991 AAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGTCAATGAGAGA 3050
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QY 3051 GTGGGGCGGAATGTTCTTAAGTCAATGTGAATGGGTTGGCAGAGAAGACTGGTGAATGCCG 3110
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QY 3171 ACCTTGTGCAGACCATCCCTGCCCTCCAGTGGCAGCTGGGGAGTGTGTCATCATGTTCTAA 3230
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US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: UNSURE

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RESULT 15

US-09-989-687-1

; Sequence 1, Application US/09989687

; Publication No. US20040002449A1

; GENERAL INFORMATION:

; APPLICANT: Hastings, Gregg A.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides

; FILE REFERENCE: 1488.107000D

; CURRENT APPLICATION NUMBER: US/09/989,687

; CURRENT FILING DATE: 2001-11-21

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: PatentIn Ver. 2.0

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; LOCATION: (1)..(2853)
; NAME/KEY: misc feature
; LOCATION: (3195)
; OTHER INFORMATION: n is any nucleic acid
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; LOCATION: (3248)
; OTHER INFORMATION: n is any nucleic acid
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Matches 2799; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Db 889 GATGAACAGAGAGGGGCCCGAAGTGAACCTCAATGTCGTCCTCACTCTGCGGAACTTTTGC 948
QY 1465 AACTGGCAGAGACGACACAAACCCACCGGAGTGCAGAGCACTATGACACAGCA 1524
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QY	1645	CAAGCTGCCCTTACACACAGCCCATGAATAGGCGACAGTGTAAATGATGCCACATGATGAT	1704
Db	1129	CAAGCTGCCCTTACACACAGCCCATGAATAGGCGACAGTGTAAATGATGCCACATGATGAT	1188
QY	1705	GCAAAGCAGTGTGCCACCTTAATGTTGTAACACAGGATTTCCACATGATGGCGTCAATG	1764
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QY	1765	CTTTCCAACTGTGACACAGCCCTTGTGTCTCTTGCAGTGGCTACATGATTAATCA	1824
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QY	1825	TTTCTCGATAATGTCATGGGGAATGTTGATGACAAAGCTCAGAAATCCCATACAGCTC	1884
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Db	1369	CCAGGCGATCTCCCTGGCACCCTGTCAGATGCCAAACCGGCGAGTCCAGTTTACATTTGGG	1428
QY	1945	GAGGACTCCAAAACCTGTCCTGATGACGACGACATGATGAGACCTTTGTGGTGTACGGGC	2004
Db	1429	GAGGACTCCAAAACCTGTCCTGATGACGACGACATGATGAGACCTTTGTGGTGTACGGGC	1488
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Db	1969	CAGCCCAAGGTTGTAGATGATGATCTCCATGTAGCCCAAGATTTCCACTGTCTGTGTGCAA	2028
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QY	2845	TACAAAGTGTGTCTTGTGAGGTACAGCGCTCTCTGCGGCAATGGAAAGAAATTCGCAGC	2904
Db	2329	TACAAAGTGTGTCTTGTGAGGTACAGCGCTCTCTGCGGCAATGGAAAGAAATTCGCAGC	2388
QY	2905	TTTAGCCCTCTCAAGAGCCCTTGCACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGA	2964
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QY	3085	TGSCAGAGAGACTGTGTAGAAATCCGAGACATTAATGGACAGCTGTCTCCGAGTGTGCA	3144
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GenCore version 5.1.6
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(without alignments)
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SUMMARIES

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3	5219	98.7	4858	3	US-09-392-184-1
4	4262	80.6	3706	3	US-09-484-970B-58
5	3922	74.2	2184	4	US-09-445-023A-2
6	3652	69.1	2184	4	US-09-445-023A-13
7	2472	46.8	2853	4	US-10-009-332-2
8	2271.5	43.0	3638	3	US-09-369-364A-8
9	2165	40.9	3126	3	US-09-392-184-7
10	2156	40.8	4192	3	US-09-122-126B-1
11	2156	40.8	4192	4	US-09-634-286A-1
12	2156	40.8	4192	4	US-10-247-685-1

13	1926.5	36.4	3250	3	US-09-122-126B-14	Sequence 14, Appl
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16	1909.5	36.1	3002	3	US-09-369-364A-1	Sequence 1, Appl
17	1751.5	33.1	5804	3	US-09-369-364A-12	Sequence 12, Appl
18	1613	30.5	2825	3	US-09-369-364A-14	Sequence 14, Appl
19	1608.5	30.4	6659	4	US-09-321-987B-1	Sequence 1, Appl
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21	1333.5	25.2	5357	3	US-09-392-184-5	Sequence 5, Appl
22	1295	24.5	3377	4	US-09-981-953A-3	Sequence 3, Appl
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36	1066.5	20.2	3160	4	US-09-963-791-25	Sequence 25, Appl
37	1040.5	19.7	1520	3	US-09-369-364A-3	Sequence 3, Appl
38	1038.5	19.6	2848	3	US-09-369-364A-4	Sequence 4, Appl
39	1003.5	19.0	3158	4	US-09-949-016-1988	Sequence 1988, Ap
40	950.5	18.0	2450	3	US-09-491-522-2	Sequence 2, Appl
41	949.5	18.0	2450	3	US-09-491-522-9	Sequence 9, Appl
42	781	14.8	1770	4	US-09-963-791-11	Sequence 11, Appl
43	718	13.6	1317	4	US-09-963-791-21	Sequence 21, Appl
44	712.5	13.5	739	3	US-09-369-364A-10	Sequence 10, Appl
45	607.5	11.5	703	3	US-09-392-184-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-130-491-1
Sequence 1, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4676
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (460)...(3360)
US-09-130-491-1

Alignment Scores:
Pred. No.: 0
Score: 5232.00
Percent Similarity: 99.38%
Best Local Similarity: 98.97%
Query Match: 98.96%
DB: 3
Length: 4676
Matches: 957
Conservative: 4
Mismatch: 6
Indels: 0
Gaps: 0

US-09-373-658C-126 (1-967) x US-09-130-491-1 (1-4676)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgAlaGlyLeuGlySerAspMetGlyAsn 20
DB 460 ATGCAAGCGAGCTGTGCGCGAGGGGTTCCGAAGCGCAGCTGGCAGCAGATGGGGAAC 519
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 520 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCGGTACCCACAGCTGCTGCTCGCC 579
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
DB 580 GCGGGGCTACTGGCGGTGTGCGAGCGACTTCGGGCGCCCTCCGAGGAGACGAGAGCTA 639
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
DB 640 GTGGTCCCGAGCTGGAGCGCCCGCGGACACGGACCCAGCGCTCCGCTCGCACGCC 699
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
DB 700 TTTGACGACGCTGGATCTGGAGCTGGCGGCGCGACAGCAGCTTTTGGCGCGCGCTTC 759
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 760 ACGCTCCGAACGTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGGAACCGACCTG 819
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 820 GCGCACTGCTTCTACTCCGGCACCGTGAATGGCATCCAGCTCGGCTCCGCCCTCAGC 879
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 880 CTCGCGAGGGCGTGGCGCGGCTTCTACTGCTGGGGGAGCGGTATTTCATCCAGCG 939
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
DB 940 CTGCGCGCGCGCAGGAGCGCTCGCCACCGCGCGCCCGCGGAGAGCGCGCGCACCA 999
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
DB 1000 CTAAGATTCCACTCTGCGCGGGGATCGGAGGGGAGCTAGGGCGGACGTGCGGGGTC 1059
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 1060 GTGGACGACGACCCCGCGCGACTGGGAAGCGGAGACCGGAAGACGAGGAGGACT 1119
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1120 GAGGGCGAGGAGGAAGGGCTCAGTGGTCCGCGCAGGACCCGCGACTGCAAGGCGTAGGA 1179
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1180 CAGCCCAACGGAACCTGGAGCATAGAAAGAGCGATTTGTGTCCAGTCCCGCTATGTG 1239
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1240 GAAACCATCTTTGGCAGACACGATCGATGGCAGAAATCCACGGCAGTGGTCTAAAGCAT 1299
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 1300 TACCTTCTCACGTTGTTTTGGTGGCAGCCAGATTGTACAAACACCCCGCAGCATTCGTAAT 1359
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 1360 TCAGTTAGCTGTGGTGTGAAGATCTTGGTCAATCCAGATGAAACAGAGGGGCGGAA 1419
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 1420 GTGACCTCAATGCTGCCCTCACTTCGCGAACTTTTGGCAACTGGCAGAGCAGCACAAAC 1479
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
DB 1480 CCACCCAGTGACGGGATCAGAGCACTATGACACAGCAATTCCTTTTCCACGACAGGAC 1539
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380

DB 1540 TTGTGTGGGTCCACAGATGTGATACTCTTGGATGGCTGATGTTGGAACTGTGTGTGAT 1599
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
DB 1600 CCGAGCAGAAGCTGCTCGTTCATAGAAGATGATGTTTACAAGCTGCCCTTCCACGAGC 1659
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 1660 CATGAATTAGGCCACGTTTAAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT 1719
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1720 AATGTTGTGAACAGGATTCACCATGATGGCGTCAATGCTTTCCAACTGGACACAGC 1779
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1780 CAGCCTTGGTCTCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGTCATGGG 1839
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1840 GAATGTTTGTGAGCAGGCTCAGAAATCCATPACAGTCCCAAGGCAATCTCCTGGCACC 1899
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1900 TCGTAGGATGCCAACCGGCGAGTCCAGTTTACATTTGGGAGGACTCCAAACACATGCCCC 1959
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1960 GATGCGAGCAGCACATGTAGCACCTTGTGTGTGTACCGGCACCTCTGTTGGGGTGTGGTG 2019
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 2020 TGTCAAAACCAACACTTCCGTTGGCGGATGGCACACAGCTGTGGAGAGGAAATGTTGT 2079
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 2080 ATCAACGGCAAGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTCATGGA 2139
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
DB 2140 AGCTGGGAATGTGGGGCTTTGGGGAGACTGTTCCAGAACGTGGCGTGGAGAGTCCAG 2199
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyrCysGluGly 600
DB 2200 TACACGATGAGGAATGTGACAAACCGCTCCCAAGAATGGAGGAGTACTGTGAAGC 2259
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 2260 AAACGAGTGGCTACAGATCTCTTAACCTTGAGGACTGTCCAGACAATAATGGAAAAAC 2319
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2320 TTTAGAGAGGAACAATGTGAAGCACACACGAGTTTTCAAAAGCTTCTTGGGAGTGGG 2379
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2380 CTTGGGTGGAATGATATCCCAAGTACGCTGGCGTCTCAACAAAGGACAGGTGCAAGCTC 2439
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2440 ATCTGCCAAGCAAAAGGCAATGGCTACTTCTTCTGTTTTCAGCCCAAGGTTGTAGATGT 2499
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
DB 2500 ACTCATGTAGCCCAAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTGGT 2559
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2560 TGTGATCGCATCATAGACTCCAAAGAGAGTTTGAATAATGTGTTGTTTGGGGGAAAT 2619
QY 721 GlySerThrCysGlyLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db 2620 GGATCTACTTTGTAATAAATATATCAGGATCATGTTACTAGTGCATAAACCCTGGATATCATGAT 2679
Qy 741 IletleThrileProThrGlyValAlaThrAsnleGluVallysGlnArgAsnGlnArgGly 760
Db 2680 ATCATCAATTCNACTGGAGCCACCAATCGAAGTGAACAGCGAACCAGAGGGGA 2739
Qy 761 SerArgenhenGlySerPheLeuAlaileLysAlaAlaAspGlyThrlyrileLeuAsn 780
Db 2740 TCCAGGAACAATGGCAGCTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAT 2799
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2800 GGTGACTACACTTTGTCCACCTTAGACCAAGACATATATGACAAAGGTGTGTCTTGAG 2859
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgTleArgSerPheSerProLeuLysGluPro 820
Db 2860 TACAGCGGCTCTCTCGGCANATTGGAAGAATTCGACAGCTTTAGCCCTCTCAAGAGCCCC 2919
Qy 821 LeuThrileGlnValLeuThrValGlyAsnAlaLeuArgProTylsileLysTyrThrTyr 840
Db 2920 TTGACCATCCAGGTTCCTTACTGTGGCAATGCCCTTCGACCTAAATTTAAATACACCTAC 2979
Qy 841 PheVallysLysLysLysGluSerPheAsnAlaileProThrPheSerAlaTrpValile 860
Db 2980 TTCGTAAGAAGAAGAGGAATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3039
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3040 GAAGAGTGGGCGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAGACTGGTAGAA 3099
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3100 TGCCGAGACATTAATGACAGCCTGCTCCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 3159
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3160 ACCAGACTTGTGTCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGGAGTGTCTCATCATGT 3219
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3220 TCTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTTGAAGTGTCTGTCCTCATATGGA 3279
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3280 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAGAAACCTTAACATTTTCATAGACTTT 3339
Qy 961 CysThrMetAlaGluCysSer 967
Db 3340 TGCACAATGGCAGAATGCAGT 3360

RESULT 2

US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.: 0 Length: 3889
Score: 5230.00 Matches: 956
Percent Similarity: 99.38% Conservatives: 5
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.92% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-568-559-1 (1-3889)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 8 ATGCAGCGATCTGTGCCCGCAGGGGTTCGGAAGCGCAAGCTGGCGACGACATGGGGAAC 67
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 68 GCGAGCGGGCTCGGGGTCTCGAGCTTTGGGCCCGTACCCAGCTGTCTGTCTGTCTGCC 127
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 128 GCGCGCTACTGGCGGTGTGCGACGCACTCGGGCGCCCTCCGAGGAGGACGAGAGCTA 187
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 188 GTGTGCGCGAGCTGGAGCGCGCCCGGAGACACGGGACACGCGCTCCGCTGCACGCC 247
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 248 TTTGACACGACGCTGGATCTGGAGCTCGGGCCCGACAGCAGCTTTTGGCGCCCGCTTC 307
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 308 ACCTCCAGAACGCTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAACACGACCTG 367
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 368 GCGCACTGTCTTACTCCGCGACCGTGAATGGCGATCCAGCTCGGCTCGCGCTCCAGC 427
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 428 CTCTGCGAGCGGTGCGCGCGCTCTTACTCTGGGGGAGGGGTATTTTATCCAGCCG 487
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 488 CTGCCCCCGCAGAGAGCGCTCGCCACCGCCCGCCCGAGGAGAGAGCCCGCGACCA 547
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
Db 548 CTACAGTTCCACCTCTCTGCGCGGAATCGGCGAGGCGACGTCGCGCGCACGTCGCGGGTC 607
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluGlyThr 220
Db 608 GTGGACACGAGCGCGCGCGCTCGGGAAGCGGAGACCCGAAAGACGAGGAGGAGACT 667
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 668 GAGGCGAGGACGAGGGGGTCTAGTGTGCGCGCAGGACCCCGCCTGCAAGGGGTAGGA 727
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 728 CAGCCACAGGAACTGGGAAGCATAAAGAGCATTTGTGTCCAGTCCAGCTCATGCTATGTG 787
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 788 GAAACCATGTTGTGGCAGACCATGTCATGGCAAAATTCACCGCAGTGGTCTTAAGGAT 847
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 848 TACCTTCTCAGTTGTTTTCGTTGGCAGCCAGATTGTACAAACACCCCGAGCATTCGTAA 907
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320

Db 908 TCAGTTAGCTGGTGGTGAAGATCTTTGGTTCATCCAGATCAACAGAAAGGGCCGGAA 967
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 968 GTGACCTCCAAATGCTGCCCTCACTCTGCGGAATCTTTGCAACTGGCAGAGCAGACAA 1027
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleuPheThrArgGlnAsp 360
Db 1028 CCACCCAGTGCACCGGATGACAGACCTATGACACAGCAATCTTTTCCACAGACGGAC 1087
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1088 TTGTGTGGGTCCACAGATGTGATATCTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1147
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1148 CCGAGCAGAAGTGTCTCCGTCTAGAGAATGATGGTTTACAAGCTGCCTTCCACACAGCC 1207
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1208 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT 1267
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1268 AATGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTGGACACACAGC 1327
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheIleuAspAsnGlyHisGly 460
Db 1328 CAGCCTTGTGCTCTCTTGGCAGTGCCTACATGATTTACATCATTTCTGGATTAATGGTCATGGG 1387
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1388 GAATGTTTATGGACAGAGCTCAGATCCATCCATACAGCTCCAGGCGATCTCCTGGCACC 1447
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1448 TCGTACGATGCCAACCGGAGTGCCTGCTTCAATTTGGGGAGGACTCCAAACACTGCCCT 1507
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyValLeuVal 520
Db 1508 GATGACGACGACACATGTAGCACCTTGTGGTGTACCGGACCTCTGTGGGGTGTGGTG 1567
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 1568 TGTCAACCAACAACTTCCCGTGGCGGATGGCACCATGCTGTGGAGAGGAAATGGTGT 1627
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCAATTTTGATACGCTTTTCATGGA 1687
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 1688 AGCTGGGAATGTGGGGCTTTGGGAGACTGTTCAGAACGTGGCGTGGAGAGTCCAG 1747
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluGly 600
Db 1748 TACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGAGTACTGTGNAGGC 1807
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 1808 AAACGAGTGGCTACAGATCTGTAACTTGAAGCTGTGAGGACTGTCCAGACAAATTAATGMAAAACC 1867
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 1868 TTTTAGAGAGGAACAATGTGAAGCACCAACGAGTTTTCAAAAGCTTCTTTGGGAGTGGG 1927
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 1928 CTGCGGTGGATGGATTTCCCAAGTACGCTGGCGTCTCCAAAGACAGAGTGCAGACTC 1987
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 1988 ATCTGCCAAGCCAAAGGCATGGCTACTCTTCTGTTTTCAGCCCCAAGGTTGTAGATGTT 2047

QY 681 ThrProCysSerSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db 2048 ACTCCATGTAGCCCCAGATTCCACCTCTGTCTGTGCAAGGACAGTGTGTAAGAGTGTGT 2107
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2108 TGTGATCGCATCATAGACTCCAAAAGAAGTTTGATTAATGTGTGTGTTTCCGGGGGAAT 2167
QY 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2168 CGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCAAAAACCTGGATATCATGAT 2227
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2228 ATCATCACAATTTCCAACTGGAGCCCAACATCAAGATGAACAGCGGAACAGAGGGGA 2287
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2288 TCCAGGAACAATGGCAGCTTTCTTGGCATCAAGCTGCTGATGGCACAATATTTCTTAAT 2347
QY 781 GlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2348 CGTGACTACACTTTGTCCACCTTAGAGCAAGACATATTGTACAAAGGTGTGTCTTGAGG 2407
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2408 TACAGCGGCTCTCTGCGGCATTTGGAAGAATTCGAGCTTTAGCCCTCTCAAGAGGCC 2467
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2468 TTGACCATCCAGTCTTACTGTGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC 2527
QY 841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2528 TTCGTAAGAAGAGAGAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2587
QY 861 GluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2588 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGCTGTGTAAGA 2647
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2648 TGCCGAGACATTAATGGACAGCTCTCTCCGAGTGTGCAAGAGAGTGAAGCCAGCCAGC 2707
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyCysLysSerCys 920
Db 2708 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 2767
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 2768 TCTAAGACCTGTGGAGAGGTTACAAAAGAAAGCTTGAAGTGTCTGCCCATGATGA 2827
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 2828 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTT 2887
QY 961 CysThrMetAlaGluCysSer 967
Db 2888 TGCACAATGGCAGAAATGCAGT 2908

RESULT 3

US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33

Db 2254 CAACAGTGGCGTACAGATCCTGTAACTTGGAGCTGTCCAGACAATAATGTAAGAAAAC 2313
Qy 620 rPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerG1 640
Db 2314 CTTTATAGAGGAAACAATGTGAAGACACACACAGATTTTCAAAAGCTTCTTTTGGGAGTGG 2373
Qy 640 yProAlaValGluTTPileProLysTyrAlaGlyValSerProLysAspArgCysLysle 660
Db 2374 GCCTGGGTGGNATGGATCCCAAGTACGCTGGCGCTTCACCAAGAGCAGAGTGCAGCT 2433
Qy 660 uileCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspG1 680
Db 2434 CATCTGCCAAGCAAGCATTTGGCTTCTTCTGTTTGGCAGCCCAAGTTGTAGATGG 2493
Qy 680 yThrProCysSerProAspSerThrSerValCysValGlnGlnGlnCysValLysAlaG1 700
Db 2494 TACTCCATGTAGCCAGATTCACCTCTCTCTGTGTGCAAGGACAGATGTGTAAAGCTGG 2553
Qy 700 yCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAs 720
Db 2554 TTGTGATCGCATATAGACTCCAAAAGAGTTTGATTAATGTGTGTTTGGCGGGGAAA 2613
Qy 720 nGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAs 740
Db 2614 TGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGA 2673
Qy 740 pileIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgG1 760
Db 2674 TATCATCAATTCACACTGGAGCCCAACCAATCGAAGTGAACAGCGCAACCAAGGGG 2733
Qy 760 ySerArgAsnAngLysSerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAs 780
Db 2734 ATCCAGGAAACAATGACAGCTTTCTTGGCCATCAAGCTGCTGATGGACATATTTCTTAA 2793
Qy 780 nGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuAr 800
Db 2794 TGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATGTAACAAAGGTGTGTCTGAG 2853
Qy 800 gTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPr 820
Db 2854 GTACAGCGGCTCTCTGGCGCATGGGAAGAATTCGCAGCTTTAGCCCTCTCAAGAGGCC 2913
Qy 820 oleuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTy 840
Db 2914 CTTGACCATCCAGGTTCTTACGTGGGCATGSCCTTCGACCTAAATTAATACACCTA 2973
Qy 840 rPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValI1 860
Db 2974 CTTGTAAAGAAAGAAGAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCA 3033
Qy 860 eGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValG1 880
Db 3034 TGAAGAGTGGGCGGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGACTGGTAGA 3093
Qy 880 uCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSe 900
Db 3094 ATGCCGAGACATTAATGGACACCTGCTTCCAGGTGTGCAAGGAAGTGAAGCCAGCCAG 3153
Qy 900 rThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCy 920
Db 3154 CACCAAGCTTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGTGTATCATG 3213
Qy 920 sSerLysThrCysGlyLysGlyTyrIlyLysThrSerLeuLysCysLeuSerHisAspG1 940
Db 3214 TTCTAAGACCTGTGGAGGGGTACAAAAAAGAGCTTGAAGTGTGTCTCCCATCATGATG 3273
Qy 940 yGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPh 960
Db 3274 AGGGTGTATCTCATGAGAGCTGTGATCTCTTTAAGAAACCTTAACATTTTCATAGACTT 3333
Qy 960 eCysThrMetAlaGluCysSer 967
Db 3334 TTGCACATGGCAGATGTCAGT 3355

RESULT 4

US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmar, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Alignment Scores:

Pred. No.:	0	Length:	3706
Score:	4262.00	Matches:	772
Percent Similarity:	99.36%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	80.61%	Indels:	1
DB:	3	Gaps:	0

US-09-373-658C-126 (1-967) x US-09-484-970B-58 (1-3706)

Qy	191	GlnGluAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys	210
Db	3	CAGGCGACGATAGGCGGACGCTGCGGGTCTGTGGACGACGAGCCCGCGGCTGGGAAA	62
Qy	211	AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer	230
Db	63	CGGAGACCGAAGACGAGGAGCTGAGGCGGAGGACGAAGGGCTCAGTGGTGG	122
Qy	231	ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys	250
Db	123	CGCAGGACCCGGCACTGCAAGCGGTAGGACAGCCCAAGGAACTGGAGGACATAAGAAAG	182
Qy	251	LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet	270
Db	183	AMGCGATTTGTCTCAGTCACCGCTATGTGGNAACCATGCTTGTGGCAGACCGAGTCGATG	242
Qy	271	AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla	290
Db	243	GCAGAAATCCACGCGCAGTGGTCTAAAGCATTAACCTTCTCACGTTGTTTTCGGTGGCAGCC	302
Qy	291	ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu	310
Db	303	AGATTGTCAAAACACCCAGCATTCGTAATTCAGTTAGCCTGCTGGTGGTGAAGATCTTG	362
Qy	311	ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg	330
Db	363	GTCAATCCAGATGAACAGAGGGGCGGAGTACCTCCATGCTGCTCTCTCTCTCTCTCTCT	422
Qy	331	AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAlaGluHisTyr	350
Db	423	AACTTTTGGCAACTGGCAGAAAGCAGCAACACCCAGTACCCGGGATGCAGGACACTAT	482
Qy	351	AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu	370
Db	483	GACACAGCAATTTCTTTTCCACAGACGAGGACTTGTGTGGTCCCGACATGTGATCTCTT	542

371 QY GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 390
543 Db GGGATGGCTGATGTTGGAAGCTGTGTGATCCGAGCAGAGAGCTGCTCCGTCATAGAAGAT 602
391 QY AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 410
603 Db GATGGTTTCAAGCTGCTCCACAGAGCCCATGAATTAGGCCACAGCTGTTTAAACATGCCA 662
411 QY HisAspAlaAlaGlyGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 430
663 Db CATGATGATGCAAGCAGTGTGCCAGCTTAAATGTTGATGCAAGGCTCCACATGATG 722
431 QY AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMet 450
723 Db GGGTCAATGCTTTCCAACTGGACACAGCAGCCCTTGGTCTCTTGGCAGTGCCTACATG 782
451 QY IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 470
783 Db ATTACATCATTTCTGGATAATGCTCATGGGAATGTTTATGATGCAAGGCTCCAGATCCC 842
471 QY IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490
843 Db ATACAGCTCCCGAGGCACTCTCCCTGGCAGCTCTGATGATGCCAACCGGAGTCCAGTTT 902
491 QY ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 510
903 Db ACATTTGGGGAGGACTCCAAACACTGCCCGCATGACAGCCAGCACATGTAGCACCTTGTGG 962
511 QY CysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAlaAsp 530
963 Db TGTACCGGACCTCTGGTGGGGTGGTGGTGTGTCAAAACCAACACTTCCCGTGGCGGAT 1022
531 QY GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHis 550
1023 Db GGCACAGCTGTGGAGAGGGAATGTTGATACAGCGCAAGTGTGAACAAACCGAC 1082
551 QY ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 570
1083 Db AGAAGCATTTTCATACGCTTTTTCATGAAGCTGGGGAATGTTGGGGCTTGGGAGAC 1142
571 QY CysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 590
1143 Db TGTTCAGAAACGTCGGTGGAGAGTCCAGTACAGATGAGGAATGTGCAACCCAGTC 1202
591 QY ProLysAsnGlyGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 610
1203 Db CCNAGAAATGGAGGAAGTACTGTGAAGCAACAGAGTGGCTACAGATCTGTAACTT 1262
611 QY GluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsn 630
1263 Db GAGGACTGTCCAGACAATAATGAAACCTTTTAGAGAGGAACAATGTGAAGCACACAAC 1322
631 QY GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 650
1323 Db GAGTGTTCAAAGCTTCTTGGAGTGGGCTCGGTGGGAATGGATTCCTCAAGTACGCT 1382
651 QY GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 670
1383 Db GGGCTCTCCAAAGGACAGTGCAGCTCATCTGCCAACCAAGGCAATGGCTACTTC 1442
671 QY PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 690
1443 Db TTCGTTTTCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTC 1502
691 QY CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 710
1503 Db TGTGTGCAAGGACAGTGTGTAAAGCTGTTGTATCGCATCATAGACTCCAAAGGAAG 1562
711 QY PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysValLysLysIleSerGlySer 730
1563 Db TTTGATAAATGTGGTGTTCGGGGGAATGGATCTACTTGTAAATAATATCAGGATCA 1622
731 QY ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 750

1623 Db GTTACTAGTGCAAAACCTGGATATCATGATATCATCAATTTCCAACTGGAGCCACAAC 1682
751 QY IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 770
1683 Db ATCGAAGTGAACAGCGGAACCGAGGGGATCCAGGAACATGCGGAGCTTCTTCCCAT 1742
770 QY elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGlu 790
1743 Db CAAAGCTGCTGATGGCACATATATTCTTAATGGTACTACACTTTGTCACCTTAGAGCA 1802
790 QY nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGlu 810
1803 Db AGACATATTATGTAAGAGGTGTTGCTGTGAGGTACAGCGCTCTCTGCGGCATTTGAAAG 1862
810 QY gIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 830
1863 Db AATTGCGACCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAA 1922
830 QY nAlaLeuArgProLysIleLysTyrThrPheValLysLysLysLysLysLysLysPheAs 850
1923 Db TGGCTTTCGACCTAAATTAATACACTTCTGTAAGAAGAGAGGAATCTTTCAA 1982
850 QY nAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCy 870
1983 Db TGCTATCCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCAATGTTCTAAGTCATG 2042
870 QY sGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 890
2043 Db TGAATTTGGGTTGGCAGAGAGACTGGTAGATGCCAGACATTAATGGACAGCTGCTTC 2102
890 QY rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 910
2103 Db CGAGTGTGCAAGGAAGTGAAGCCAGCCAGCAGACCTTGTGCAGACCATCCCTGCC 2162
910 QY oGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 930
2163 Db CCAGTGGCAGCTGGGGAGTGGTCACTGTTCTTAAGACCTGTGGGAAGGTTACAAAA 2222
930 QY sThrSerLeuLysCysLeuSerHisAspGlyValLeuLeuSerHisAspSerCysAspPr 950
2223 Db AGAAGCTTGAAGTGTCTGTCCATCATGAGGGGTGTTATCTCATGAGAGCTGTGATCC 2282
950 QY oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
2283 Db TTTTAAAGAAACCTTAAACATTTTCATAGACTTTTGCACATGGCAGGAATGCAAT 2334

RESULT 5

US-09-445-023A-2
Sequence 2, Application US/09445023A
Patent No. 6565858

GENERAL INFORMATION:

- APPLICANT: Hirose, Kunitaka
- APPLICANT: Inoguchi, Eiichi
- APPLICANT: Hakozaaki, Michinori
- APPLICANT: Ishioka, Keiko
- APPLICANT: Ishida, Yukako
- APPLICANT: Matsushima, Kouji
- APPLICANT: Kuno, Kouji

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
FILE REFERENCE: Q57092

CURRENT FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: JP 9-160422

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patent in version 3.0

SEQ ID NO 2

LENGTH: 2184

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

QY 908 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 927
DB 2002 CCTGCCCCCAGTGGCAGCTGGGGAGTGGTTCATCATGTTCTAAGACCTGTGGGAGGCT 2061
QY 928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947
DB 2062 TACAAAAAAGAGCTTGAAGTGTCTGTCCTCCATGATGGAGGGGTGTATCTCATGAGAGC 2121
QY 948 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
DB 2122 TGTGATCCTTTTAAAGAAACCTAAACATTTCTAGACTTTTTCACACTGACAGTGCAT 2181

RESULT 6
US-09-445-023A-13
Sequence 13, Application US/09445023A
Patent No. 6565858
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Biiji
APPLICANT: Hakozaaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical.
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445, 023A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 2184
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.: 0 Length: 2184
Score: 3652.00 Matches: 646
Percent Similarity: 94.77% Conservatives: 43
Best Local Similarity: 88.86% Mismatches: 38
Query Match: 69.08% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-445-023A-13 (1-2184)

QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1 AAGCCATCAGGACGAGCAGCATAAGAGAGAGCGATTTGTGTCCAGCCCCCGTTATGTG 60
QY 261 GluThrMetLeuValalaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 61 GAAACCATGCTCGTAGCTGACCGAGTCATGGCCGAGTTCCAGCGCAGCGGTCTAAAGCAT 120
QY 281 TyrLeuLeuThrLeuPheSerValalaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 121 TACCTTCTAACCTGTCTCGGTGGCAGCCAGCTTTTACAGCATCCAGCATTTAGGAAT 180
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 181 TCAATTAGCCTGTGTGTGTGAAGATCTTGGTCTATATACGAGGAGGAGGAGCCAGAA 240
QY 321 ValThrSerAsnAlaalaLeuThrLeuAtcAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 241 GTTACCTCCAATGAGCTCTCACCCCTTCGGAAATTTCTGCGAGTGGCAGAAACCAAC 300
QY 341 ProProSerArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360

DB 301 AGCCCCAGTGCAGCGGATCCAGAGCAGCTATGACACTGCAATTCGTGTCCAGACAGGAT 360
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
DB 361 TTATGTGGCTCCACACAGGTGACACTCTCGGAATGGCAGATGTTGGACACCTGATGTGAC 420
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
DB 421 CCCAGCAGGAGCTGTCTCAGTCATAGAGATGATGGTTTGCAGCTGCCCTTCCACACAGCC 480
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 481 CATGAATTGGGCCATGTGTTTAAACATGCCCGCAGATGATGCTAAGCAGCTGTGCACCTTG 540
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 541 AATGTGTGAGTGGCGATTTCTCATGTATGGCTCGATGCTCTCCAGCTTAGACCATAGC 600
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 601 CAGCCCTGGTCACTTGCAGTGCCTACATGGTCAAGCTCCTCTCTGATCTTCCCGGTACC 720
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 661 GAATGTTGATGGACAAGCCAGATCCCAATCAAGCTCCTCTCTGATCTTCCCGGTACC 720
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 721 TTGTAGTAGTCCCAACCCGAGTGTCAAGTTCATTCGAGAGAGAAATCCAGACACTGCCCT 780
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 781 GATGAGCCAGCAGCATGTACTACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 841 TGCCAAACAAACACTTCCCTTTGGGAGATGGCAGCAGCTGTGGAGAGGAAAGTGGTGT 900
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 901 GTCAGTGGCAGTGTGCTGAACAGACAGACATGAGCATTTTGTCTACTCTCTGTTCTAGGA 960
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
DB 961 AGCTGGGACCATGGGACCGTGGGAGACTGTCTCAAGAACCTGTGGTGGTGGAGTTCMA 1020
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
DB 1021 TACCAATGAGAGATGTGACCAACCCAGTCCCAAGAACGAGGAGGAGTACTCTGTGAAGGC 1080
QY 601 LysAtqValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 1081 AAACGAGTCCGCTACAGGTCTGTATACATCGAGACTGTCCAGACATTAACGGAAACG 1140
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 1141 TTCAGAGAGGAGCAGTGGCAGCGCAGCAATGAGTTTTTCCAAAGCTTCTTTGGGAATGAG 1200
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 1201 CCCACTGTAGAGTGGACACCCAGTACCGCGCGCTCTCGCCAAAGGACAGTGCAGCTC 1260
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 1261 ACCTGTGAAGCCAAAGCATTTGGCTACTTTTCTCTTACAGCCCAAGGTTGTAGATGGC 1320
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
DB 1321 ACTCCCTGTAGTCCAGACTCTACTCTGTGTGTGTGCAAGGGCAGTGTGTGAAAGCTGGC 1380
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720

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Db 1381 TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGTATAGTGTGGCGTTTGTGGAGAAAC 1440
Qy 721 GlySerThrCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 740
Db 1441 GGTTCACATCAGAGAGATGTCTAGGAATAGTCTAGTACAGACCTGGGTATCATGAC 1500
Qy 741 IleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 1501 ATTGTACAAATCTCTGTGGAGCACCAACATGTAAGTGAACATCGGATCAAGGGGG 1560
Qy 761 SerArgAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 1561 TCCAGAAACAATGCGAGCTTCTCGCTATTATGAGCGGCTGATGCTACCTATATCTGAAT 1620
Qy 781 GlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 1621 GGAACACTTCACTCTGTGCACACTAGAGCAAGACCTCACTCAAGAGTACTGTCTTAAGG 1680
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 1681 TACAGTGGTTCCTCGCTGCGCTGGAGAGATCCGACGTTTGTACCTCAAGAACCC 1740
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 1741 TTAACCATCCAGGTTCTTATGTTAGGCCATGCTCTCCGACCAAAATTAATTTACCTTAC 1800
Qy 841 PheValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 860
Db 1801 TTTATGAAGAAGAAGACAGAGTCAATCAACGCCATTCCTCCATTTTCTGAGTGGGTGATT 1860
Qy 861 GluGluTyrGlyGluCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGlu 880
Db 1861 GAAGATGGGGGAGTGTCTCAAGACATCGCGTCAGGTTGGCAGAGAGTAGTAGCAG 1920
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 1921 TGCAGAGACATTAACGGACACCTGCTTCCGAATGTGCAAGAGAGTCAAGCCAGCAGT 1980
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTyrGlnLeuGlyGluTyrSerSerCys 920
Db 1981 ACCAGACCTTGTGCAGACCTTCTCTTGGCCACACTGGCAGGTTGGGGGATTTGTTCACCATGT 2040
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 2041 TCCAAACCTTGGGGAAGGTTTACAGAGAGACCTTGAATGTGTCTCCACAGTGG 2100
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 2101 GGCCTGTATTCAATGAGAGCTGTGATCCTTTGAAGAGCAAGCAATACATTGACTTTT 2160
Qy 961 CysThrMetAlaGluCysSer 967
Db 2161 TGCACACTGCACACAGTGCAGT 2181
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RESULT 7

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US-10-009-332-2
; Sequence 2, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2853
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-332-2
Alignment Scores:
Pred. No.: 2e-217 Length: 2853
Score: 2472.00 Matches: 487
Percent Similarity: 64.18% Conservative: 149
Best Local Similarity: 49.14% Mismatches: 256
DB: 46.76% Indels: 99
DB: 4 Gaps: 22
US-09-373-658c-126 (1-967) x US-10-009-332-2 (1-2853)
Qy 36 LeuLeuLeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGlu 55
Db 1 ATGCTTTTGTGGGCATCTTAACCTTGCTTTCGCGGGGAAACCGCTGGAGGCTTTGAG 60
Qy 56 GluAspGluGluLeuValPro---GluLeuGlu----- 66
Db 61 CCAGAGCGGGAGGTAGTCTTCCATCCGACTGGACCGGACATTAAACGGCGCGCTTAC 120
Qy 67 -----ArgValPro-----GlyHisGlyThrArgLeuArgLeuHisAlaPhe 81
Db 121 TACTGGCGGGGTCCGAGGACTCCGCGGATCAGGAGCTCAFTTTTTCAGATCACAGATT 180
Qy 82 AspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPheThr 101
Db 181 CAGAGAGACTTTTACCTACCTACCTGACCGCGGATGCTCAGTTCTTGGCTCCCGCTTCTCC 240
Qy 102 LeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuPro----- 116
Db 241 ACTGAGCATCTGGGC-----GTCCCTCTCCAGGGGCTCACCGGGGGC 282
Qy 117 GluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAla 136
Db 283 TCTTCAGACCTTCGACGCTGCTTCTATTCGGGACGCTGAACCGGACCTCGGACTTCGTTTC 342
Qy 137 AlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyr 156
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Qy 157 PheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLys 176
Db 403 GTCAATTAGCCGCTGCCAATGCTAGC-----GGCGCGGGCGCGCAGCGCAACAGC 453
Qy 177 ProProAlaProLeuGlnPheHisLeuLeuArg-----AsnArgGln 191
Db 454 CAGGGCGCA-----CACCTTCTCCAGCGCGGGGTGTTCGGGGCGGGCTTCC 501
Qy 192 GlyAspValGlyGlyThrCysGlyValValAspAsp---GluProArg---ProThrGlyL 210
Db 502 GGAGACCCACCTCTCGCTGGGGGTGGCTCGGGCTGGAAACCGCCCATCTACGGGGC 561
Qy 210 ysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrps 230
Db 562 CTGGACCCCTTACAAGCGCGCGGGGCTTCGGGGAGAG----- 602
Qy 230 erProGlnAspProAla-LeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 249
Db 603 -----TCGTAGCGCGCGCAGGTCTGGG-----CGC 627
Qy 250 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 269
Db 628 GCCAAGCGTTTCTGTGTCTATCCCGGGTACGTGGAGAGCGTGGTGTCTCGGACGAGTCA 687
Qy 270 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 289
Db 688 ATGGTCAAGTTTCCACGGCGCGACCTCGAACAATTATCTGCTGACGCTGTGTGCAACGGCG 747
Qy 290 AlaArgLeuTyrLysHisProSerIleArgSerValSerLeuValValValValVal 309
Db 748 GCGCGACTTACCGGCCATCCAGCATCTCTCAACCCCATCAATCGTTGTGTGTCAGGTG 807
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310 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaIleLeuThrLeu 329
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Db CGTCTTCTAGAGATCGTGAATCCGGGCCCAAGGTCAACGGCCATGGGGCCCTGACGCTG 867

330 ArgAspPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 349
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370 LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu 389
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Db CTGGGCATGGCTGATGTGGTACCATCTGTGACCCCAAGAGAAGCTCTCTGTCAATTGAG 1047

390 AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGlnLeuGlyHisValPheAsnMet 409
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Db GACGATGGGCTTCCATCAGCCTTCAACCTGCCACGAGCTGGGGCCACGCTGTTCACCATG 1107

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| | | | | : : : : :
Db CCCATGACAAATGAAAGTCTGTGAGGAGGTGTTGGGAAGCTCCGAGCCACCAACATG 1167

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| | | | | : : : : :
Db ATGTCCCCGACCTTCATCCAGATCGACCGTGCACACCCCTGTGTGCTGCTGCTGCC 1227

450 MetIleThrSerPheLeuAspAsnGlyHisGlyCysLeuMetAspLysProGlnAsn 469
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510 TrpCysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAla 529
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668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
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688 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 707
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| | | | | : : : : :
Db AGAAGAGATTCGACAAAGTGTGGGTGTGTGGGGAGACAAATAGAGCTCAAGAAGAGTG 2055

728 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 747
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768 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 787
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808 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 827
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853 ProThrPheSer-----AlaTrpValIle 860
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| | | | | : : : : :
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918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
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| | | | | : : : : :
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958 IleAspPheCysThrMetAlaGluCys 966
| | | | | : : : : :
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RESULT 8
US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:

; APPLICANT: Apte, Suneel
 ; APPLICANT: Hurskainen, Tiina L.
 ; APPLICANT: Hirohata, Satoshi
 ; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
 ; FILE REFERENCE: 26473/4007/10-30-00
 ; CURRENT APPLICATION NUMBER: US/09/369,364A
 ; CURRENT FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 3638
 ; TYPE: DNA
 ; ORGANISM: Mus musculus ADAMTS-8
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (278)..(2992)
 ; NAME/KEY: misc feature
 ; LOCATION: (3636)
 ; OTHER INFORMATION: n = T
 ; US-09-369-364A-8



Alignment Scores:
 Pred. No.: 9,27e-199 Length: 3638
 Score: 2271.50 Matches: 452
 Percent Similarity: 61.66% Conservative: 151
 Best Local Similarity: 46.22% Mismatches: 288
 Query Match: 42.96% Indels: 87
 DB: 3 Gaps: 22

US-09-373-658c-126 (1-967) x US-09-369-364A-8 (1-3638)

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DB 263 CAGCACTCGCCCCCATGCTCGCGGACCCACCACCACCGGGTGGCGGCCCTCTCTGCTG 322
QY 39 LeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSer-----54
DB 323 CTGCTATTGCAGCTGCGCGCGCGCCACTCGCTCGGAGCCCGCGCGCGCGGAGCC 382
QY 55 ---GluGluAspGluGluLeuValProGluLeuGluArgValProGlyHisGlyThr 73
DB 383 GGGGCGCAGGCTCGAGAGTAGTGGTGGCC-----ACGCGGTTCGCGCGAGCGCGGAGC 436
QY 74 ---ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProAsp 92
DB 437 GAGCTCGCCTTCACCTGTCGCGCTTCGCGCAGGGCTTCGCTCGCGCTCGCGCTGAC 496
QY 93 SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAsp 112
DB 497 GCCAGCTTCCTGGCGCGGAAATCAAGATCGAGCGCTCGGGGGTTCGAGCGCGCGGCC 556
QY 113 ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp 132
DB 557 GGG-----GGCGAGCGCGGAGTAGCTGCTGCTCTCTCTGCGCACAGTAATGAGAA 610
QY 133 ProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeu 152
DB 611 CGGGAGTCGCTGGCGCGGATGAGCTGTGTCGCGGGTGGAGCGGCTCGTCTCTGCTGGA 670
QY 153 GlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer-----GluArg 167
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QY 168 LeuAlaThrAlaAlaProGlyGluLysPro-----177
DB 731 CTGCGCGCTGGGGCGCGGAGCGCCCGGAGACCCCGGCTCGCTCGCGCGGAGTT 790
QY 178 -----ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspVal 194
  
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DB 848 -----GAGAGAAAT 856
QY 215 AspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspPro 234
DB 857 GACAACGAGGAGGACAAAGACGAGGAGGGGTGCTCAAGAGACACAGAGACTCC 916
QY 235 AlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheVal 254
DB 917 -----CGCAAGTGCACCACTTCGATCC---AAACTAGAACGACAGAGTTTGTG 967
QY 255 SerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHis 274
DB 968 TCCGAGGCTCGCTTCGTGAAACACTTCTGTGGTGGTGCATGCGTCCATGGCTTCAT 1027
QY 275 GlySerGlyLeuLysHisTyrLeuThrPheSerValAlaAlaArgLeuTyrLys 294
DB 1028 GGGACCGACTGCAGAACCATCTCAGGTGATGTCATGCGACCGCCGATCTACAG 1087
QY 295 HisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAsp 314
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QY 528 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 547
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RESULT 9
US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 3126
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3126)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
US-09-392-184-7

Alignment Scores:
Pred. No.: 4.8e-189 Length: 3126
Score: 2165.00 Matches: 443
Percent Similarity: 62.49% Conservative: 140
Best Local Similarity: 47.48% Mismatches: 246
Query Match: 40.95% Indels: 106
DB: 3 Gaps: 24
US-09-373-658c-126 (1-967) x US-09-392-184-7 (1-3126)

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QY 96 LeuAlaProGlyPheThrLeuGlnAsnVal-----GlyArgLysSerGlySerAsp 112
Db 3056 CTGGCGCCGACTTCAAGATCGAGCGCTTCGGGGGCTCCGGCGCGCGCGCGGGGC--- 3000
QY 113 ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp 132
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QY 287 rValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVa 307
Db 2535 TGTGGCAGCCCGAATCTACAGCACCCAGCATCAAGAAATTCATCACTGATGGTGT 2476
QY 307 llystleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLe 327
Db 2475 AAAAGTGTGATCGTAGAAGATGAATAATGGGGCCCGAGGTGTCGACAAATGGGGGCT 2416
QY 327 uThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisenProProSerAspArgAspAl 347
Db 2415 TACACTGGGTAACTTCTGCACTGGCAGCGCGGTTCACACCGCCAGCGACCCGCCACC 2356
QY 347 aGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGln---Th 366
Db 2355 AGAGCACTACGACAGCGGCATCTCTCTCACCAGACAGAACTTCTGTGGCGAGGGGCT 2296
QY 366 rCysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSe 386
Db 2295 GTGTGACACCTGGGTGTGGCAGACATCGGACCATTTGTGACCCCAACAAAGCTGTCT 2236
QY 386 rValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisVa 406
Db 2235 CGTGATCGAGGATGAGGGGCTCCAGCGCGCCACACCTCGGCCCACTGAAGTGGGCGCT 2176
QY 406 lPheAsnMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAs 426
Db 2175 CTTAGCATGCCACGACGATCTCCAGCCCTGCACACGGCTCTTCGGGCCCATGGGCA 2116
QY 426 pSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpTrpSerProCy 446
Db 2115 GCACACGCTGATGGCACCGCTGTCTCCACCTGAACACAGACGCTGCCCTGCTGCCCTG 2056
QY 446 sSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHis-----G1 460
Db 2055 CAGCCCGCATGTATCTCACAGAGCTTCTTACGGGGGGCCACCGATTCAGTATTATGGC 1996
QY 460 yGluCysLeu-MetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyT 480
Db 1995 CTTGTGTCTAGGTG----- 1982
QY 480 hrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysP 500
Db 1981 -----CTACAGCGTTCATATGCTCTTTGGCGGATTTCCGCCACTGCG 1936
QY 500 roAsp-----AlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyV 518
Db 1935 CCAACACCTCTCTCAGGACGCTCGCGCCAGCTTTGGTGC---CACACTGATGGGGCTG 1879
QY 518 aLeuValCysGlnThrLysHis-----PheProTrpAlaAspGlyThrSerCysGlyG 536
Db 1878 AGCCCTGTGCCACAGAAATGGCAGCTGCTGCGCTGCGGCTGACGCGACCGCTGGGGC 1819
QY 536 luGlyLysTrpCysIleAsnGlyLys-CysValAsnLysAsnHisArgLysHisPheAsp 555
Db 1818 CTGGGCACCTCTCTCAGAAAGGCAAGCTGTCTACCTGAGGAGAGTGGAGAGGCCCAAG 1759
QY 556 ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpTrpGlyAspCysSerArgThrCys 575
Db 1758 CCCGTGGTATGAGGGCTGGGCACCGTGGGACCCCTGGGAGAAATGTTCTCGACCTGT 1699
QY 576 GlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGly 595

Db 1698 GGAGGAGGATACAGTTTTCACCGTGAAGCAAGGACCCGAGCTTCAGAAATGGAGGA 1639
QY 596 LysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAsp 615
Db 1638 AGATACTGCTCGGGTCGAGAGACCAAGTACCAGTATGCCACGAGGAATGCCCCCT 1579
QY 616 AsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAla 635
Db 1578 ---GACGGGAAGCTTCAGGGAGCAGCAGTGTGAGAAGTATATGCTCACAATTACACT 1522
QY 636 SerPheGlySerGlyProAlaValGluTrpLeuProLysTyrAlaGlyValSerProLys 655
Db 1521 GACATG---GACGGGAATCTCTGCACTGGGTCCCAAGTATGCTGGGTGTGCCCGGG 1465
QY 656 AspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnPro 675
Db 1464 GACCGCTCAAGTGTCTGCGGAGCCCGGGGAGGACGAGTTCAAAAGTGTTCGAGGCC 1405
QY 676 LysValValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGln 695
Db 1404 AAGGTGATTGATGGCACCTGTGTGGGCAGAAACACTGGCCATCTGTCTCGTGGCCAG 1345
QY 696 CysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGly 715
Db 1344 TGTGTCAAGGCGCGCTGTGACCATGTGTGGACTCGCTCGGAAGCTGCACAAATGCGGG 1285
QY 716 ValCysGlyGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLys 735
Db 1284 GTGTGTGGGGCAAAAGCAACTCTTCGAGGAAGGTCTCCGGTCTCCACCCCCACCAAT 1225
QY 736 ProGlyTyrHisAspIleThrIleProThrGlyAlaThrAsnIleGluValLysGln 755
Db 1224 TATGCTACATGACATTTGTCACCATCCAGCTGTGGCCACTAATATTGACGTGAAGCAG 1165
QY 756 ArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGly 775
Db 1164 CGGAGCCACCGGGTGTGCAGAACCATGGGAACCTACCTGGCGCTGAAGACGCTGATGG 1105
QY 776 ThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLys 795
Db 1104 CAGTACCTGTCTCAACGGCAACTGGCCATCTCTGCCATAGACAGACATCTTGTGTGAG 1045
QY 796 GlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSer 815
Db 1044 GGGACCATCTCTGAAGTACAGCGCTCCATCGCCACCTCGAGCGCTGCAGAGCTTCGG 985
QY 816 ProLeuLysGluProLeuThrIleGlnValLeuThrVal---GlyAsnAlaLeuArgPro 834
Db 984 CCGTTGCCAGAGCGCTCTGACAGTGCAGCTCTCTGACAGTCCCTGGCGAGGTCTTCCCCCA 925
QY 835 LysIleLysTyrThrTyrPheVal-----LysLys 844
Db 924 AAAGTCAAAATACACTCTTTGTTCTCTAATGACGTGGACTTTAGCATGCAGAGCAGCAAA 865
QY 845 LysLysGluSerPheAsnAlaIle---ProThrPheSerAla---TrpValIleGluGlu 862
Db 864 GAGAGGACCAACCAACCATCATCCAGCGCTGTCTCCAGCAGACGTGGGTGTGGGGAC 805
QY 863 TrpGlyGluCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGluCysArg 882
Db 804 TGGTCTGAGTGTCTTAGCACCTTCGCGGGCGCGCTGGCAGAGCGCAACTGTAGAGTGCAG 745
QY 883 AspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArg 902
Db 744 GACCCCTCGGCGACGCTCTGCCCCTGTGATTCAGGGGGCAGGGGCCAGTCTTGTGCTC 685
QY 903 ProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSer---CysSe 921
Db 684 CCTCGGAAGCCAGCTGTGCCCTGTGATTCAGGGGGCAGGGGCCAGTCTTGTGCTC 625
QY 921 rLysThrCysGlyLysGlyTyrLysLysThrSerLeuLys----- 934

Db 624 CTGGACATGCGGT-----ACTGAGGTGCACACAGGGTCTCCACTGTGGT 580
Qy 935 -----CysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLy 952
Db 579 GACTGGTCTCTGGCCATAT-CAAGGCACACAGGCCCCACCCAGGCGTC---CAATGGCC 524
Qy 952 sLysProLyHisPheIleAspPheCysThr 962
Db 523 GCAACCC-----CTCCAGTACTGCACA 502

RESULT 10
US-09-122-126B-1
; Sequence 1, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-122-126B-1

Alignment Scores:
Pred. No.: 5,26e-188 Length: 4192
Score: 2156.00 Matches: 450
Percent Similarity: 60.55% Conservative: 144
Best Local Similarity: 45.87% Mismatches: 281
Query Match: 40.78% Indels: 109
DB: 3 Gaps: 26

US-09-373-658c-126 (1-967) x US-09-122-126B-1 (1-4192)

Qy 7 GluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluAlaProGly 26
Db 432 GAGGGGCTGGCAGGGCGCTGGTGT-GGGAGGCCAACCTCTCTCTCTCTCTCTCTCT 490
Qy 27 SerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaLeuAlaVal 46
Db 491 TGCGGCT 546
Qy 47 SerAspAlaLeuGlyArgProSerGluGluAspGluLeuValValProGluLeu--- 65
Db 547 TCAGCCCGCTGGCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606
Qy 66 -----GluArgValProGlyHisGlyThr---ThrArgLeu-----ArgLeuHisAla 80
Db 607 AACGGCAGCT 666
Qy 81 PheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAlaProGlyPhe 100
Db 667 TTTGGGAGAGCGTGTACTAGAGCTGGAGCAGGACTCCCGTGTGCGAGGTGCGAGGGCTG 726
Qy 101 ThrLeuGlnAsnValGlyArgLys-----SerGlySerAspThrProLeuPro 116
Db 727 ACAGTGCAGTACCTTGGCCAGCGCCCTGAGTGTCTGGTGGAGCAGAG-----CCT 777
Qy 117 GluThrAspLeuAlaHisCysPheTySerGlyThrValAsnGlyAspProSerAla 136
Db 778 GGCACC-----TACCTGACTGGCACCACATCAATGGAGATCCGAGTGGTG 822
Qy 137 AlaAlaLeuSerLeuCysGluGly---ValArgGlyAlaPheTyLeuLeuGlyGluAla 155
Db 823 GCATCTGTCACTGGGATGGGGAGCCCTGTGTAGGCGTGTGTACAAATATCGGGGGCTGAA 882

Qy 156 TyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlu 175
Db 883 CTCCACTCTCAGGCCCTGGAGGAGGAGCCCTAACTCTGCT---GGGGACCTGGGGCT 939
Qy 176 LysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGly 195
Db 940 -----CACATCTTACGCCGGAAG----- 957
Qy 196 GlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAsp 215
Db 957 ----- 957
Qy 216 GluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAla 235
Db 958 -----AGTCTGCCAGCGGTCAAGGTCTCCATGTGCAACGTCAAGGTCTCT--- 1002
Qy 236 LeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSer 255
Db 1003 -----CTTGAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 1050
Qy 256 SerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGly 275
Db 1051 CTGAGTAGATTGTGGAGACACTGGTGTGGCAGATGACAAAGATGCCCGCATTCACGGT 1110
Qy 276 SerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHis 295
Db 1111 GCGGGGCTAAAGCGCTACTCTGCTAAAGTGTGGCAGCAGCAGCAGCAGCAGCAGCAGC 1170
Qy 296 ProSerIleArgAsnSerValSerLeuValValValValValValValValValVal 315
Db 1171 CCAAGCATCGCAATCTGTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1230
Qy 316 GlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrp 335
Db 1231 GAGGAGGGGCCCCAAGTGGGGCCAGTGTCTGCCAGACCTCTGGCAGCTTCTGTGCTGG 1290
Qy 336 GlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeu 355
Db 1291 CAGCGGGGCTCAACACCCCTGAGGACTCGGACCTCGACCTTTGACACAGCAGCAGCAT 1350
Qy 356 PheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspVal 375
Db 1351 TTTACCGCTCAGACCTGTGTGGTGTCTCCACTTGGCAGCAGCTGGTGGTGGTGGTGGT 1410
Qy 376 GlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAla 395
Db 1411 GGACCGCTGTGTACCGCGCTCGAGCTGTGCCATTTGGAGGATGTGGCTCCAGTCA 1470
Qy 396 AlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLys 415
Db 1471 GCCTTCACTGCTCTCATGAATGGGTCTATGTCTTCAACATGTCTCCATGACCACTCCA 1530
Qy 416 GlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHisMetMetAlaSerMetLeu 434
Db 1531 CCATGATCATGTGTGAATGGGCTTTGAGCAGCCTCTCGCCATGTCTGGGCGCTGTGATG 1590
Qy 435 SerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPhe 454
Db 1591 GCTCATGTGTGATCTCGAGGAGCCCTGTGTCCTCTGAGTGGCCGCTTCATCAGTACT 1650
Qy 455 LeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuPro 474
Db 1651 CTGGACAATGGTATGGGCACTGTCTCTTAGACAAACACAGAGGCTCCATTTGCATCTGC 1710
Qy 475 GlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGlu 494
Db 1711 GTGACTTTCTCCGTGAGGACTATGATGTGACCGCCAGTGGCAGCTGACCTTCGGGGCC 1770
Qy 495 AspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThr 514
Db 1771 GACTCAGCCATTTGTCCACAGCTGGCCCGCCCTGTGCTGCTGCTGCTGCTGCTGCTG 1830
Qy 515 SerGlyGlyValLeuValCysGlnThrLysPhePheProTrpAlaAspGlyThrSerCys 534

Db 1471 GCCTTCACTGCTGCTCATGAATGGGTGCTGCTTCAACATGCTCCATGACAACTCCCAAG 1530
Qy 416 GlnCysAlaSerLeuAenGly---ValAsnGlnAspSerHisMetMetAlaSerMetLeu 434
Db 1531 CCATGCAATGATGTTGAATGGCCCTTTCAGGACCTCTCGCCATGTCATGGCCCTCTGTATG 1590
Qy 435 SerAsnLeuAspHisSerGlnProTTPSerProCysSerGlyTyrMetIleThrSerPhe 454
Db 1591 GCTCATGTGATCTGAGGAGCCCTGTCTCCCTGTCAGTGGCCGCTTCATCATCTGACTTC 1650
Qy 455 LeuAspAenGlyHisGlyGluCysLeuMetAspLysProGlnAenProIleGlnLeuPro 474
Db 1651 CTGCAATGCTATGGCCACTGTCTCTTAGACAAACACAGAGGCTCCATTGTCATCTGCCT 1710
Qy 475 GlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGlu 494
Db 1711 GTGATTTTCCCTGGCAAGGACTATGATGCTAGCCGCGGAGTGCAGCTTCCTGGGCC 1770
Qy 495 AspSerLysHisCysProAspAlaAspThrCysSerThrLeuTyrCysThrGlyThr 514
Db 1771 GACTCAGCCATTGTCACAGCTCCCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1830
Qy 515 SerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCys 534
Db 1831 CTCAATGGCCATGCTGTCACAGCTCCCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1890
Qy 535 GlyGluClyLysTrpCysIleAenGlyLysCysValAsnLysAsnHisAsgLysHisPhe 554
Db 1891 GGGCCCGCACAGGCTGCATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1950
Qy 555 AspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThr 574
Db 1951 AATATTCCACAGGCTGCTGCTGGGTGCTTGGGGACCATGGGTGCTGCTGCTGCTGCTG 2010
Qy 575 CysGlyGlyGlyValGlnTrpMetArgGluCysAspAenProValProLysAsnGly 594
Db 2011 TGTGGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2070
Qy 595 GlyLysTrpCysGluClyLysArgValArgTyrArgSerCysAenLeuGluAapCysPro 614
Db 2071 GGCAGTACTGTGAGGGCCCGCTACCCGCTTCCGCTTCCGCAACATCGAGGAGCTGCCCA 2130
Qy 615 AspAsnAenGlyLysThrPheArgGluGlnCysGluAlaHisAenGluPheSerLys 634
Db 2131 ACTGGCTCAGCCCTGACTTCCGAGGAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG 2190
Qy 635 AlaSerPheGlySerGlyProAla---ValGluTrpIleProLysTyrAlaGlyValSer 653
Db 2191 CTC---TTCAAGAGCTTCCAGGGCCCATGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 2247
Qy 654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673
Db 2248 CCCAGGACCATGTCAACTCACCTGCGAGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTG 2307
Qy 674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db 2308 GAGCCAGGGTGTGTAGTGGAGCCCTTGTTCCTCCGAGACAGCTCTCTGGTCTGTGTCAG 2367
Qy 694 GlyGlnCysValLysAlaGlyCysAspArgIleAenAspSerLysLysLysPheAspLys 713
Db 2368 GGCCGATGATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2427
Qy 714 CysGlyValCysGlyLysGlnSerThrCysLysLysIleSerGlySerValThrSer 733
Db 2428 TGCAATGTTGTCGGAGGGGACGGTTCGTGTTGACAGCAAGCATGCTCCCTCAGGAAA 2487
Qy 734 AlaLysProGlyTyrHisAspIleIleThrProThrGlyAlaThrAsnIleGluVal 753
Db 2488 TTCAGGTACGGATACAAATGTTGGTCACTATCCCGGGGGGCCACCCACATCTTGTGTC 2547
Qy 754 LysGlnArgAenGlnArgGlySerArgAsnAenGlySerPheLeuAlaIleLysAlaAla 773

Db 2548 CGCAGCAGCGGAAACCCCTGGCCACCGGAGC-----ATCTACTTGGCCCTCGAAGCTGCCA 2601
Qy 774 AspGlyThrTyrIleLeuAenGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793
Db 2602 GATGGCTCTATGCTCCATCATGATGATGATACACGCTGATGCTCCCTCCACAGATGTGTA 2661
Qy 794 TyrLysGlyValVal---LeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArg 812
Db 2662 CTGCTGGGGCAGTCACTGCTGCTACAGCGGGGCCACTGCAGCCTCAGAGACACTGTCA 2721
Qy 813 SerPheSerProLysGluProLeuThrIleGlnValLeuThrValGlyAenAlaLeu 832
Db 2722 GGCATGGGCCACTGGCCGCTTTCACATCTGACATCTGAGTCTCTAGTGGTGGCAACCCCCAG 2781
Qy 833 ArgProLysIleLysTyrThrPheValLysLysLysGluSerPheAsnAlaIle 852
Db 2782 GACACAGCCTCCGATACAGTCTTCTGTCGCCCGCGCCGACCTTCA---ACGCCACGC 2838
Qy 853 ProThrPheSerAlaTrpVal-IleGluGlu-----Trp----- 863
Db 2839 CCCACTCCCGAGACTGGCTGCACCGAAGACACAGATCTTGGAGATCTTGGCGCGCGC 2898
Qy 864 ----GlyGluCysSer----- 870
Db 2899 CCTGGCGCGGACAGAAATACCTCACTATCCCGGCTGCCCTTCTTGGGCACCGGGCGCT 2958
Qy 870 sGluLeuGlyTrpGlnArgArg-----LeuValGluCysArgAspIleAsnGly 886
Db 2959 CGACTTAGCTGGAGAAAGAGAGAGCTTCTGTGTGCTGCTCATGCTTAAGACTCAGTGGG 3018
Qy 886 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 906
Db 3019 GAGG-----GGCTGGCGGTGAGACTGCGCCCTCTCTGCTGCTTAATCGCAGG 3069
Qy 906 pHisProCysPro-----GlnTrpGln-----LeuGlyGluTrpSerSerCysSe 921
Db 3070 CTGGCCCTGCGCTGGTTCCTGCGCTGGGAGGAGTATGATGGTGTAGTGGATGGAAG--GG 3127
Qy 921 xLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGlyVl 941
Db 3128 GCTGACAGACAGCCCTCCATCTAAACCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTG 3187
Qy 941 Y 941
Db 3188 G 3188

RESULT 13

US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
; US-09-122-126B-14

Alignment Scores:
Pred. No.: 5,09e-167 Length: 3250
Score: 1926.50 Matches: 400
Percent Similarity: 53.53% Conservative: 123
Best Local Similarity: 40.94% Mismatches: 325
Query Match: 36.44% Indels: 130

DB:	3	Gaps:	18	
US-09-373-658c-126 (1-967) x US-09-122-126B-14 (1-3250)				
QY	5	ValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArg-Al 24		
DB	156	GTTCCGCTCCCTGGCCGC-----GGTCGGCCCGCCGCGAC 194		
QY	24	aProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaLeuLeu 44		
DB	195	ACCTGCCAGGATAAGCGCGCAGCTCCGACT-----GCTGC 233		
QY	44	uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValValProG1 64		
DB	234	AGCAGCGCCAGCCCCCGCGCGAGGGGAGAGGTGACGAGCGAGCGCGCCT-- 291		
QY	64	uLeuGluArgValProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPh 81		
DB	292	-----CCCGGCCACCCGACCCCTGGCGCAGCGCGCAGGCAAGGGGCT 338		
QY	81	eAspGlnGlnLeuAsp----- 86		
DB	339	GGTGCAACATCGACCACTACTCCGCGCGCGCAAGGTGGGTACTCTGCTACGC 398		
QY	87	-----LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100		
DB	399	GGCGCGCGGAGGTCTCTTGAGCTGGAGCGAGATGGTTCGGTGGGCAATTGCTGGCTT 458		
QY	100	eThrLeuGlnAenValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120		
DB	459	CGTG-----CCGCGAGCGCGCGAGTGGCGCTCGCGCCCTCGCGCTGTCTTGA 560		
QY	120	uAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSe 140		
DB	501	GAGCACTCTTCTATCGGGGACACGTGACGCTAGTCCCGCTCTCTGGCTGTCTTGA 560		
QY	140	rLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheileGlnPr 160		
DB	561	CCTCTGTGGGGTCTCGACGGCTTCTTCGGGTCAAGCAGCGCGGTACACCTAAGGCC 620		
QY	160	oLeu-----ProAlaAlaSerGlu----- 166		
DB	621	ACTGTGCGCGACCTCGCGCGAGGAGAAAGGGCGCGGTACGGGGATGGTCCGC 680		
QY	167	-ArgLeu-AlaThrAla-----AlaP 173		
DB	681	ACGGATCTCTGCACGTCTACACCGCGAGGGCTTCAGCTTCGAGGCGCTGCCCGCGCGC 740		
QY	173	roGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyA 193		
DB	741	CAGCTGCGAACCCTCCGCTCCA----- 763		
QY	193	spValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGluT 213		
DB	764	-----CACCGAGGCGCCACGAGCATGCTCCGCG 791		
QY	213	hrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnA 233		
DB	792	GC-----ACAGCAACCCGAGCGGACGCGCAGCACTGG-----CCTCGCA 830		
QY	233	spProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----GlySerI 248		
DB	831	GCTCTGGACCACTCGCTCTCTCGCCCTCGCTGGGGCTCAGGACCGACAGCTGGTGGCG 890		
QY	248	leArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspG 268		
DB	891	G-CGGCGCGCGCTCCATCTCCCGCGCGCCAGGTGGAGTGTCTGTGTGGCTGAGC 949		
QY	268	lnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerV 288		
DB	950	CGTCCATGGCGGTGTATGGCGGGGCTCGACGATTAACCTGTGACCCCTGGCTCCA 1009		
QY	288	aAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 308		
DB	1010	TCGCCAATAGCTGTACAGCCATGCTAGCATCGAAGAACCATCCGCTGGCCGTGTGA 1069		
QY	308	yslleLeuVallleHisAspGluGlnLysGlyProGluValThrSerAsnAlaLeuT 328		
DB	1070	AGGTGGTGTGTAGCGCAAGGACAGAGCTGGAAGTGGAGCAAGCGTGCCACCA 1129		
QY	328	hrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaG 348		
DB	1130	CACTCAGAACCTTTTGCAGGTGGCAGCACCAACACACACAGCTGGGAGATGACCATGAG 1189		
QY	348	luHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysA 368		
DB	1190	AGCACTACGATGCAGCTATCTGTTTACTCGGGAGATTATGTGGCATCATTCATGTG 1249		
QY	368	spThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValI 388		
DB	1250	ACACCTGGGAATGGCAGCGTGGGACCATATGTTCTCCAGAGCGCAGCTGTGTGTGA 1309		
QY	388	leGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheA 408		
DB	1310	TGGAAGAGATGGCCTCCAGCGCCTTCACTGTGGCTCACGAATCGGACATTTACTTGT 1369		
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US-09-634-286A-14
? Sequence 14, Application US/09634286A
? Patent No. 6521436
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company
? TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
? FILE REFERENCE: DM6909A
? CURRENT APPLICATION NUMBER: US/09/634,286A
? CURRENT FILING DATE: 2000-08-09
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 14
? LENGTH: 3250
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (121)..(2910)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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(without alignments)
3110.277 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	5232	99.0	967	14	US-10-115-286-2
4	5232	99.0	967	16	US-10-757-450-2
5	5224	98.8	967	16	US-10-755-889-134
6	5224	98.8	967	17	US-10-741-600-1603
7	5224	98.8	967	17	US-10-741-600-1604
8	5221.5	98.8	968	10	US-09-373-658-125
9	5144	97.3	950	11	US-09-373-658-2
10	5144	97.3	950	11	US-09-989-687-2
11	5140	97.2	949	17	US-10-667-281-2
12	5136	97.1	950	17	US-10-741-600-1605
13	5036	95.3	931	9	US-09-741-151-4

14	4293.5	81.2	968	13	US-10-163-316-7	Sequence 7, Appli
15	4293.5	81.2	968	16	US-10-391-364-82	Sequence 82, Appli
16	4264.5	80.7	951	15	US-10-381-793-3	Sequence 3, Appli
17	4260.5	80.6	950	9	US-09-321-987B-4	Sequence 4, Appli
18	3922	74.2	727	9	US-09-445-023A-1	Sequence 1, Appli
19	3922	74.2	727	14	US-10-097-597-1	Sequence 1, Appli
20	3922	74.2	727	14	US-10-097-580-1	Sequence 1, Appli
21	3656	69.2	727	9	US-09-445-023A-12	Sequence 12, Appli
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23	3656	69.2	727	14	US-10-097-580-12	Sequence 12, Appli
24	3303	62.5	608	9	US-09-803-589-2	Sequence 2, Appli
25	3297	62.4	608	9	US-09-803-589-8	Sequence 8, Appli
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ALIGNMENTS

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; Sequence 126, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 967
; TYPE: PRT
; ORGANISM: ITGL-TSP
US-09-989-687-126

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; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; CURRENT FILING DATE: 2002-03-25
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIORITY FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIORITY FILING DATE: EARLIER FILING DATE: 1997-09-05
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; LENGTH: 967
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; ORGANISM: Homo sapiens
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Query Match 99.0%; Score 5232; DB 13; Length 967;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 957; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 MORAVPEGFGRRKLGSDMGNAERAPGSRSGFVPPTLLLLAALLAVSDALGRPSSEDEL 60
Db 1 MORAVPEGFGRRKLGSDMGNAERAPGSRSGFVPPTLLLLAALLAVSDALGRPSSEDEL 60
Qy 61 VPELERYPGHGTTRRLRHLAFDQQLDLRDPSSFLAPGFTLQNVGRKSGSETPLPETDL 120
Db 61 VPELERYPGHGTTRRLRHLAFDQQLDLRDPSSFLAPGFTLQNVGRKSGSETPLPETDL 120
Qy 121 AHCFFYSGTVNGDPPSSAAALSLCEGVGAFYLLIGRAYFTOPLPAASERLATAAGKPPAP 180
Db 121 AHCFFYSGTVNGDPPSSAAALSLCEGVGAFYLLIGRAYFTOPLPAASERLATAAGKPPAP 180
Qy 181 LQFHLRRNRQDVGTCGVVDDEPRPTGKAEDEDEGTEGDEGPOWSPDPAQGVG 240
Db 181 LQFHLRRNRQDVGTCGVVDDEPRPTGKAEDEDEGTEGDEGPOWSPDPAQGVG 240
Qy 241 QPTGTGSIKRRKRVSSHRVETMLVADQSMAEFHGSLGKHYLLTLFSAARLYKHPISRN 300
Db 241 QPTGTGSIKRRKRVSSHRVETMLVADQSMAEFHGSLGKHYLLTLFSAARLYKHPISRN 300
Qy 301 SVSLVVKLVTHDQKQPEVTSNAALTLRNFQKQKQHNPPSDRDAEYDTAILFTQD 360
Db 301 SVSLVVKLVTHDQKQPEVTSNAALTLRNFQKQKQHNPPSDRDAEYDTAILFTQD 360
Qy 361 LCGSQTCDTLGADVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACSL 420
Db 361 LCGSQTCDTLGADVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACSL 420
Qy 421 NGVNQDSHMAASMLNLDHSPWSPCSGYMTSFLDNGHGECLMDKQNPQIQLPGLPQT 480
Db 421 NGVNQDSHMAASMLNLDHSPWSPCSGYMTSFLDNGHGECLMDKQNPQIQLPGLPQT 480
Qy 481 SYDANROCOFTGEDSKHCPDAASTCSTLWCTGTSGGVLCOTKHPHADGTSCEGKWC 540
Db 481 SYDANROCOFTGEDSKHCPDAASTCSTLWCTGTSGGVLCOTKHPHADGTSCEGKWC 540
Qy 541 INKCVNKNHRKHFTDPFHGSGMWGMPWGDSCSRTCGGVQVYTMRECDNPPVKNKGKCYCBG 600
Db 541 INKCVNKNHRKHFTDPFHGSGMWGMPWGDSCSRTCGGVQVYTMRECDNPPVKNKGKCYCBG 600
Qy 601 KRVRYSNLEDCPDNNGKTFREEQCEAHNEFSPKASFGSGPAVEWIPKYAGVSPKDRCKL 660
Db 601 KRVRYSNLEDCPDNNGKTFREEQCEAHNEFSPKASFGSGPAVEWIPKYAGVSPKDRCKL 660
Qy 661 ICQAKGIGYFFVLQPKVVDGTPCSPDSTSVQGVQCVKAGCDRIIDSXKKPKCGVCGN 720
Db 661 ICQAKGIGYFFVLQPKVVDGTPCSPDSTSVQGVQCVKAGCDRIIDSXKKPKCGVCGN 720
Qy 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQNRQSGRNNGSFLAIAKAADGTIYN 780
Db 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQNRQSGRNNGSFLAIAKAADGTIYN 780
Qy 781 GDTLSTLEQDQIMYKGVVLYSGSSAALERSFSPKLEPLTIQVLTGNALRPKIKYTY 840
Db 781 GDTLSTLEQDQIMYKGVVLYSGSSAALERSFSPKLEPLTIQVLTGNALRPKIKYTY 840
Qy 841 FVKKKESFNALPTFSAWVIEWGECSKCELGWQRRLLVECRDINGQPAEACEKVPKAS 900
Db 841 FVKKKESFNALPTFSAWVIEWGECSKCELGWQRRLLVECRDINGQPAEACEKVPKAS 900
Qy 901 TRPCADHPCPQWLGEWSSCSKTCGKYKTSKLSLCLSHDGGVLSHDSCDPLKPKHFIDF 960
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Db 901 TRFCADHPCPQWLGWSSCKTCGKGYKRSKLKCLSHDGGVLSHSCDPLKPKHIDF 960

Qy 961 CTWAECS 967

Db 961 CTWAECS 967

RESULT 3

US-10-115-286-2
; Sequence 2, Application US/10115286
; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 967 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-115-286-2

Query Match 99.0%; Score 5232; DB 14; Length 967;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 957; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MQRAVPGFGRKLGSDMGNAERAPGSRFGPVTLLLLAAALLAVSDALGRPSDEEL 60
Db 1 MQRAVPGFGRKLGSDMGNAERAPGSRFGPVTLLLLAAALLAVSDALGRPSDEEL 60
Qy 61 VVPELERVPGHGTTRLRHAFDQQLDLDPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
Db 61 VVPELERVPGHGTTRLRHAFDQQLDLDPDSSFLAPGFTLQNVGRKSGSETLPETDL 120
Qy 121 AHCFYSGTVNGDPSSAAALSICEGVGAFYLLGAYFIQPLPAASERLATAAPGKPPAP 180
Db 121 AHCFYSGTVNGDPSSAAALSICEGVGAFYLLGAYFIQPLPAASERLATAAPGKPPAP 180

Qy 181 LQFHLLRRNRQGDVGTCGVDDDEPRPTGKAETEDDEGTEGDEGQWSPQDPALQGVG 240
Db 181 LQFHLLRRNRQGDVGTCGVDDDEPRPTGKAETEDDEGTEGDEGQWSPQDPALQGVG 240
Qy 241 OPTGTGSIIRKGRFVSSHRYVETMLVADQSMAPGSLGKHYLLTLFSVAARLYKHSIRN 300
Db 241 OPTGTGSIIRKGRFVSSHRYVETMLVADQSMAPGSLGKHYLLTLFSVAARLYKHSIRN 300
Qy 301 SVSLVVVKILVIHDEQKPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTROD 360
Db 301 SVSLVVVKILVIHDEQKPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTROD 360
Qy 361 LCGSQCTDLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASL 420
Db 361 LCGSQCTDLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASL 420
Qy 421 NGVNDQSHMWASMLSNLDHSQWSPSCGYMITSFLONGHGECLMDKPNQPIQLPGDLPGT 480
Db 421 NGVNDQSHMWASMLSNLDHSQWSPSCGYMITSFLONGHGECLMDKPNQPIQLPGDLPGT 480
Qy 481 SYDANRQCQFTFGEDSKHCPDAASTCTSLWCTCTSGGLVVCQTKHFPWADGTSCGEGKWC 540
Db 481 SYDANRQCQFTFGEDSKHCPDAASTCTSLWCTCTSGGLVVCQTKHFPWADGTSCGEGKWC 540
Qy 541 INKCVNKNHRKHFDPFHGSMGWGPGWDCSRTCGGVQVYTWRECDNPVPKNGKTCYCEG 600
Db 541 INKCVNKNHRKHFDPFHGSMGWGPGWDCSRTCGGVQVYTWRECDNPVPKNGKTCYCEG 600
Qy 601 KRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSAKSGSPAVEMIPKYAGVSPKDRCKL 660
Db 601 KRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSAKSGSPAVEMIPKYAGVSPKDRCKL 660
Qy 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFDRKCGVCGN 720
Db 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFDRKCGVCGN 720
Qy 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQRNQRNNGSFLATKAADGTYILN 780
Db 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQRNQRNNGSFLATKAADGTYILN 780
Qy 781 GDYTLSTLEQDINMYGVVLYRSGSSAALRIRSFPLKEPLTIQVLTGVALRPKIKYTY 840
Db 781 GDYTLSTLEQDINMYGVVLYRSGSSAALRIRSFPLKEPLTIQVLTGVALRPKIKYTY 840
Qy 841 FVKKKESFNAIPTFSAWVIEEWGECSSCELGWQRRLVECRDINGOPASECAKEVPAS 900
Db 841 FVKKKESFNAIPTFSAWVIEEWGECSSCELGWQRRLVECRDINGOPASECAKEVPAS 900
Qy 901 TRPCADHPCPQWLGWSSCKTCGKGYKTSKLKCLSHDGGVLSHSCDPLKPKHIDF 960
Db 901 TRPCADHPCPQWLGWSSCKTCGKGYKTSKLKCLSHDGGVLSHSCDPLKPKHIDF 960
Qy 961 CTWAECS 967
Db 961 CTWAECS 967

RESULT 4
US-10-757-450-2
; Sequence 2, Application US/10757450
; Publication No. US20040175794A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge


```
181 LQPHLLRRNRQDVGCTCGVDDDEPRPTGKAETEDDEGTEGEDEGPQMSPODPALQGVG 240
181 LQPHLLRRNRQDVGCTCGVDDDEPRPTGKAETEDDEGTEGEDEGPQMSPODPALQGVG 240
241 QPTGTGSIIRKGRFVSHRIVETMLVADQSMABPHGSLGKHYLLTLFSAARLYKHPISRN 300
241 QPTGTGSIIRKGRFVSHRIVETMLVADQSMABPHGSLGKHYLLTLFSAARLYKHPISRN 300
301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
361 LCGSQCTDLTGADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
361 LCGSQCTDLTGADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
421 NGVNQDSHMAWMLSNLDHSPWSPCSGYMTITSFLDNHGHGECMLDKPQNPQIQLPGDLPGT 480
421 NGVNQDSHMAWMLSNLDHSPWSPCSGYMTITSFLDNHGHGECMLDKPQNPQIQLPGDLPGT 480
481 SYDANRQCFTFGEDSKHCPDAASTCTLWCTGSGVLVCOQKHPWADGTSCEGKWC 540
481 SYDANRQCFTFGEDSKHCPDAASTCTLWCTGSGVLVCOQKHPWADGTSCEGKWC 540
541 INKCVNKNRKHFDTPFHGSMGWGPDGDCSRTCGGVQYVYTMRECDNPVPKNGKGYCEG 600
541 INKCVNKNRKHFDTPFHGSMGWGPDGDCSRTCGGVQYVYTMRECDNPVPKNGKGYCEG 600
601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKSGPAVEWIPKYAGVSPKDRCKL 660
601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKSGPAVEWIPKYAGVSPKDRCKL 660
661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCXGN 720
661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCXGN 720
721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTIYLN 780
721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTIYLN 780
781 GDTLSTLEQDIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
781 GDTLSTLEQDIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
961 CTMAECS 967
961 CTMAECS 967
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RESULT 6

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US-10-741-600-1603
; Sequence 1603, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1603
; LENGTH: 967
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-600-1603
Query Match 98.8%; Score 5224; DB 17; Length 967;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 956; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 MORAYPEGFGRRKLGSDMGNAERAPGSRSGFVPVPTLLLLAALLAVSDALGRPSEDEEL 60
DB 1 MORAYPEGFGRRKLGSDMGNAERAPGSRSGFVPVPTLLLLAALLAVSDALGRPSEDEEL 60
QY 61 VVPELERVPGHGTTRILRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
DB 61 VVPELERVPGHGTTRILRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
QY 121 AHCFYSGTVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAAGEKPPAP 180
DB 121 AHCFYSGTVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAAGEKPPAP 180
QY 181 LQPHLLRRNRQDVGCTCGVDDDEPRPTGKAETEDDEGTEGEDEGPQMSPODPALQGVG 240
DB 181 LQPHLLRRNRQDVGCTCGVDDDEPRPTGKAETEDDEGTEGEDEGPQMSPODPALQGVG 240
QY 241 QPTGTGSIIRKGRFVSHRIVETMLVADQSMABPHGSLGKHYLLTLFSAARLYKHPISRN 300
DB 241 QPTGTGSIIRKGRFVSHRIVETMLVADQSMABPHGSLGKHYLLTLFSAARLYKHPISRN 300
QY 301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
DB 301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
QY 361 LCGSQCTDLTGADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
DB 361 LCGSQCTDLTGADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
QY 421 NGVNQDSHMAWMLSNLDHSPWSPCSGYMTITSFLDNHGHGECMLDKPQNPQIQLPGDLPGT 480
DB 421 NGVNQDSHMAWMLSNLDHSPWSPCSGYMTITSFLDNHGHGECMLDKPQNPQIQLPGDLPGT 480
QY 481 SYDANRQCFTFGEDSKHCPDAASTCTLWCTGSGVLVCOQKHPWADGTSCEGKWC 540
DB 481 SYDANRQCFTFGEDSKHCPDAASTCTLWCTGSGVLVCOQKHPWADGTSCEGKWC 540
QY 541 INKCVNKNRKHFDTPFHGSMGWGPDGDCSRTCGGVQYVYTMRECDNPVPKNGKGYCEG 600
DB 541 INKCVNKNRKHFDTPFHGSMGWGPDGDCSRTCGGVQYVYTMRECDNPVPKNGKGYCEG 600
QY 601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKSGPAVEWIPKYAGVSPKDRCKL 660
DB 601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKSGPAVEWIPKYAGVSPKDRCKL 660
QY 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCXGN 720
DB 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCXGN 720
QY 721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTIYLN 780
DB 721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTIYLN 780
QY 781 GDTLSTLEQDIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
DB 781 GDTLSTLEQDIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
QY 841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
DB 841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
QY 901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
DB 901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
QY 961 CTMAECS 967
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Db          961 CTMAECS 967
|||||
RESULT 7
US-10-741-600-1604
; Sequence 1604, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1604
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1604

Query Match      98.8%; Score 5224; DB 17; Length 967;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 956; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
Db 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
QY 61 VVPELERVPGHGTTTRLRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
Db 61 VVPELERAPGHGTTTRLRHAFDQQLDLDLRPOSSFLAPGFTLQNVGRKSGSETLPETDL 120
QY 121 AHCFSYGTGVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP 180
Db 121 AHCFSYGTGVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP 180
QY 181 LQFHLLRRNQDVGTCGVVDDEPRPTGKAETDEDETEDEGEGPQSPDPAALQGVG 240
Db 181 LQFHLLRRNQDVGTCGVVDDEPRPTGKAETDEDETEDEGEGPQSPDPAALQGVG 240
QY 241 OPTGTGSRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFSVAARLYKHPISR 300
Db 241 OPTGTGSRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFSVAARLYKHPISR 300
QY 301 SVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTROD 360
Db 301 SVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTROD 360
QY 361 LCGSQTCDTLGMADVTCVDPSSCSVIEDDGLQAAFTTAHLGHVFNPHDADAKQCSAL 420
Db 361 LCGSQTCDTLGMADVTCVDPSSCSVIEDDGLQAAFTTAHLGHVFNPHDADAKQCSAL 420
QY 421 NGVNQDSHMAWNLNLDHSPWSPCSGYMTITSFLDNGHGECMLDKPQNPICLPGLDPT 480
Db 421 NGVNQDSHMAWNLNLDHSPWSPCSGYMTITSFLDNGHGECMLDKPQNPICLPGLDPT 480
QY 481 SYDANRQCOFTFEGDSKHCPDAASTCSTLWCTGTSGGVLVLCOTKHPWADGTCGEGKWC 540
Db 481 SYDANRQCOFTFEGDSKHCPDAASTCSTLWCTGTSGGVLVLCOTKHPWADGTCGEGKWC 540
QY 541 INKCKVKNRKHFDTPFHSGVMGMPWGDGCSRTCGGVQYVTRMRECDNPVKNQKCYCBG 600
Db 541 INKCKVKNRKHFDTPFHSGVMGMPWGDGCSRTCGGVQYVTRMRECDNPVKNQKCYCBG 600
QY 601 KVRVRSNLEDCPNNGKTFREOCEAHNEFSKASFGSGPAVEWPKYAGVSPKORCKL 660
Db 601 KVRVRSNLEDCPNNGKTFREOCEAHNEFSKASFGSGPAVEWPKYAGVSPKORCKL 660
QY 661 ICAQKIGIGYFFVLQPKVVDGTPCSPDSTSVQVQGVKAGCDRIIDSKKKPKDCKGVCNG 720
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Db          961 CTMAECS 967
|||||
RESULT 8
US-09-373-658-125
; Sequence 125, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 125
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-125

Query Match      98.8%; Score 5221.5; DB 10; Length 968;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 957; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 59
Db 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
QY 60 LVVPELERVPGHGTTTRLRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETD 119
Db 61 LVVPELERAPGHGTTTRLRHAFDQQLDLDLRPOSSFLAPGFTLQNVGRKSGSETLPETD 120
QY 120 LAHCFYSYGTGVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPA 179
Db 121 LAHCFYSYGTGVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPA 180
QY 180 PLOFHLLRRNQDVGTCGVVDDEPRPTGKAETDEDETEDEGEGPQSPDPAALQGV 239
Db 181 PLOFHLLRRNQDVGTCGVVDDEPRPTGKAETDEDETEDEGEGPQSPDPAALQGV 240
QY 240 GQPTGTGSRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFSVAARLYKHPISR 299
Db 241 GQPTGTGSRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFSVAARLYKHPISR 300
QY 300 NSVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTRO 359
|||||
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Db 301 NSVSLVVVKKILVIHDEQKPEVTSNAALTIRNFCNWKQHNPSPDRDAEHYDTAILFTRQ 360
QY 360 DLCSGTCOTLGNADVGTCDPERSCSVIEDDGLQAAFTTAHGLGVFNPHDADAKQAS 419
Db 361 DLCSGTCOTLGNADVGTCDPERSCSVIEDDGLQAAFTTAHGLGVFNPHDADAKQAS 420
QY 420 LNVGVNDSHMMASMLNLDHSPQSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLFG 479
Db 421 LNVGVNDSHMMASMLNLDHSPQSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLFG 480
QY 480 TSYDANRQCOFTFGEDSKHCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKW 539
Db 481 TSYDANRQCOFTFGEDSKHCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKW 540
QY 540 CINGKCVNKHRRKHFDTPPHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGKYCE 599
Db 541 CINGKCVNKHRRKHFDTPPHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGKYCE 600
QY 600 GKRVYRSCNLEDCPONNGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCK 659
Db 601 GKRVYRSCNLEDCPONNGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCK 660
QY 660 LICOAKGIGYFVFLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGG 719
Db 661 LICOAKGIGYFVFLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGG 720
QY 720 NGSTCKKISGSVTSAPGVHDIITPTGATNIEVKQNRQSGRNGSFLAKAADGTIYL 779
Db 721 NGSTCKKISGSVTSAPGVHDIITPTGATNIEVKQNRQSGRNGSFLAKAADGTIYL 780
QY 780 NGDYTLSTLEQDIMYKGVLRYSGSSAALIRISFSPLKEPLTIQVLTVGNALRPKIKYT 839
Db 781 NGDYTLSTLEQDIMYKGVLRYSGSSAALIRISFSPLKEPLTIQVLTVGNALRPKIKYT 840
QY 840 YFVKKKESFNAIPTFSAWIEBWGECSSKSELGWQRLVECRDINGQPASECAKEVKA 899
Db 841 YFVKKKESFNAIPTFSAWIEBWGECSSKSELGWQRLVECRDINGQPASECAKEVKA 900
QY 900 STRPCADHPCPQWLGEWSSCKTCGKYKTSILKCLSHDGVLSHDSCDPLKKPKHFID 959
Db 901 STRPCADHPCPQWLGEWSSCKTCGKYKTSILKCLSHDGVLSHDSCDPLKKPKHFID 960
QY 960 FCTMAECS 967
Db 961 FCTMAECS 968

RESULT 9

US-09-373-658-2
; Sequence 2, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-2
Query Match 97.3%; Score 5144; DB 10; Length 950;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 940; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 18 MGNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRSEDEELVPELERVPGHGTTLR 77
Db 1 MGNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRSEDEELVPELERVPGHGTTLR 60
QY 78 LHAFOQDLDDLVPPSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFYSGTVNGDPSAA 137
Db 61 LHAFOQDLLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSGTVNGDPSAA 120
QY 138 ALSLCGVGGAFFLLGEAYFIQPLPAASERLATAAPEGKPPAPLOPHLLRRNRQGVGGT 197
Db 121 ALSLCGVGGAFFLLGEAYFIQPLPAASERLATAAPEGKPPAPLOPHLLRRNRQGVGGT 180
QY 198 CGVVDDEPRTGKAETDEDETEGDEGPQSPDPAALQGVQPTGTGTSIRKRFVSSH 257
Db 181 CGVVDDEPRTGKAETDEDETEGDEGPQSPDPAALQGVQPTGTGTSIRKRFVSSH 240
QY 258 RYVETMLVADQSMABFHGSLGHYLLTLFSVAARLYKHPISIRNSVSLVWVKILVIHDEQK 317
Db 241 RYVETMLVADQSMABFHGSLGHYLLTLFSVAARLYKHPISIRNSVSLVWVKILVIHDEQK 300
QY 318 GPEVTSNAALTIRNFCNWKQHNPSPDRDAEHYDTAILFTRQDLCSGOTCDTLGMADVGT 377
Db 301 GPEVTSNAALTIRNFCNWKQHNPSPDRDAEHYDTAILFTRQDLCSGOTCDTLGMADVGT 360
QY 378 VCDPSSRCSVIEDDGLQAAFTTAHGLGVFNPHDADAKQASLNGVNDSHMMASMLSNL 437
Db 361 VCDPSSRCSVIEDDGLQAAFTTAHGLGVFNPHDADAKQASLNGVNDSHMMASMLSNL 420
QY 438 DHSQPSPCSGYMITSFLLNGHGECLMDKPNPIQLPGDLPGTSDYANRQCOFTFGEDSK 497
Db 421 DHSQPSPCSGYMITSFLLNGHGECLMDKPNPIQLPGDLPGTSDYANRQCOFTFGEDSK 480
QY 498 HCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKWCINGKCVNKHRRKHFDT 557
Db 481 HCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKWCINGKCVNKHRRKHFDT 540
QY 558 FHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGKYCEGKRVYRSCNLEDCPDNN 617
Db 541 FHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGKYCEGKRVYRSCNLEDCPDNN 600
QY 618 GKTFFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFVFLQPKV 677
Db 601 GKTFFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFVFLQPKV 660
QY 678 VDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGNGSTCKKISGSVTSAPG 737
Db 661 VDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGNGSTCKKISGSVTSAPG 720
QY 738 YHDIITPTGATNIEVKQNRQSGRNGSFLAKAADGTIYLNGDYTLSTLEQDIMYKV 797
Db 721 YHDIITPTGATNIEVKQNRQSGRNGSFLAKAADGTIYLNGDYTLSTLEQDIMYKV 780
QY 798 VLRYSGSSAALIRISFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKGSFNAIPTFSA 857
Db 781 VLRYSGSSAALIRISFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKGSFNAIPTFSA 840
QY 858 WVIIEWGECSSKSELGWQRLVECRDINGQPASECAKEVKAPEPCADHPCPQWLGEW 917
Db 841 WVIIEWGECSSKSELGWQRLVECRDINGQPASECAKEVKAPEPCADHPCPQWLGEW 900
QY 918 SSCSKTCGKYKTSILKCLSHDGVLSHDSCDPLKKPKHFIDFCTMAECS 967
Db 901 SSCSKTCGKYKTSILKCLSHDGVLSHDSCDPLKKPKHFIDFCTMAECS 950

RESULT 10

US-09-989-687-2
; Sequence 2, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.

APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
FILE REFERENCE: 1488.107000D
CURRENT APPLICATION NUMBER: US/09/989,687
CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 950
TYPE: PRT
ORGANISM: Homo sapiens
US-09-989-687-2

Query Match
Best Local Similarity 97.3%; Score 5144; DB 11; Length 950;
Matches 940; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 18 MGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 77
DB 1 MGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 60

QY 78 LHAFOQDLVDVPPSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAA 137
DB 1 LHAFOQDLVDVPPSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAA 120

QY 138 ALSLCGVRGAFYLLGEAFIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGST 197
DB 121 ALSLCGVRGAFYLLGEAFIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGST 180

QY 198 CGVVDDEPRPTGKAETDEDETEDEGEDEGPQSPDPAQGVQPTGTGSIKRRKFVSSH 257
DB 181 CGVVDDEPRPTGKAETDEDETEDEGEDEGPQSPDPAQGVQPTGTGSIKRRKFVSSH 240

QY 258 RYVETMLVADQSMABFHSGLKHYLLTLFSAARLYKHPISIRNSVSLVVKLLVHDEQK 317
DB 241 RYVETMLVADQSMABFHSGLKHYLLTLFSAARLYKHPISIRNSVSLVVKLLVHDEQK 300

QY 318 GPEVTSNAALTLRNFCNWKQHNPPSDRAEHYDTAILFTRQDLCSQTCDTLGMADVGT 377
DB 301 GPEVTSNAALTLRNFCNWKQHNPPSDRAEHYDTAILFTRQDLCSQTCDTLGMADVGT 360

QY 378 VCDPSRCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSNL 437
DB 361 VCDPSRCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSNL 420

QY 438 DHSQWSPCSGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 497
DB 421 DHSQWSPCSGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 480

QY 498 HCPDAASTCTLWCTGTSGVLVVCOTKHPFPAWADGTSCEGKWCINGKCNKXNRKHFDT 557
DB 481 HCPDAASTCTLWCTGTSGVLVVCOTKHPFPAWADGTSCEGKWCINGKCNKXNRKHFDT 540

QY 558 FHSGWGMGPWDCSRTCGGVQYTMRECDNPPVKNNGKCYCEGKRVYRSCNLEDCPDNN 617
DB 541 FHSGWGMGPWDCSRTCGGVQYTMRECDNPPVKNNGKCYCEGKRVYRSCNLEDCPDNN 600

QY 618 GKTFFREQEAINBFSKASFGSGPAVEWIPKYGAVSPKDRCKLIQAKGIGYFFVLQPKY 677
DB 601 GKTFFREQEAINBFSKASFGSGPAVEWIPKYGAVSPKDRCKLIQAKGIGYFFVLQPKY 660

QY 678 VDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFKDKCGVCGNGSTCKKISGSVTSKAPG 737
DB 661 VDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFKDKCGVCGNGSTCKKISGSVTSKAPG 720

QY 738 YHDIITPTGATNIEVKQRNQRSGRNGSFLLAKAADGTYYILNGDYTLSTLEQDIMYKGV 797
DB 721 YHDIITPTGATNIEVKQRNQRSGRNGSFLLAKAADGTYYILNGDYTLSTLEQDIMYKGV 780

QY 798 VLRYSGSSAALRIRISFSPLEPLTQVLTGNALRPKIKYTFVKKKESFNALPTPSA 857
DB 781 VLRYSGSSAALRIRISFSPLEPLTQVLTGNALRPKIKYTFVKKKESFNALPTPSA 840

QY 858 WVIREWGSCSKSELGMORRLVECRDINGOPASECAKEVKPASTRPACADHPCPQOLGEM 917
DB 841 WVIREWGSCSKSELGMORRLVECRDINGOPASECAKEVKPASTRPACADHPCPQOLGEM 900

QY 918 SSCSKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKPHFIDFCTMAECS 967
DB 901 SSCSKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKPHFIDFCTMAECS 950

RESULT 11
US-10-667-281-2
Sequence 2, Application US/10667281
Publication No. US20050100916A1
GENERAL INFORMATION:
APPLICANT: Klonowski, Paul
APPLICANT: Allard, John
APPLICANT: Heller, Renu
TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
TITLE OF INVENTION: Compositions Encoding the Same
FILE REFERENCE: ROCH-002
CURRENT APPLICATION NUMBER: US/10/667,281
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/09/568,559
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 60/133,343
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 949
TYPE: PRT
ORGANISM: human
US-10-667-281-2

Query Match
Best Local Similarity 97.2%; Score 5140; DB 17; Length 949;
Matches 939; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 19 GNAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 78
DB 1 GNAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 60

QY 79 HAFDQDLVDVPPSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAAA 138
DB 61 HAFDQDLVDVPPSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAAA 120

QY 139 LSLCEGVRGAFYLLGEAFIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGSTC 198
DB 121 LSLCEGVRGAFYLLGEAFIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGSTC 180

QY 199 GVVDDEPRPTGKAETDEDETEDEGEDEGPQSPDPAQGVQPTGTGSIKRRKFVSSH 258
DB 181 GVVDDEPRPTGKAETDEDETEDEGEDEGPQSPDPAQGVQPTGTGSIKRRKFVSSH 240

QY 259 YVETMLVADQSMABFHSGLKHYLLTLFSAARLYKHPISIRNSVSLVVKLLVHDEQK 318
DB 241 YVETMLVADQSMABFHSGLKHYLLTLFSAARLYKHPISIRNSVSLVVKLLVHDEQK 300

QY 319 PEVTSNAALTLRNFCNWKQHNPPSDRAEHYDTAILFTRQDLCSQTCDTLGMADVGT 378
DB 301 PEVTSNAALTLRNFCNWKQHNPPSDRAEHYDTAILFTRQDLCSQTCDTLGMADVGT 360

QY 379 CDPSRCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSNL 438
DB 361 CDPSRCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSNL 420

QY 439 HSQWSPCSGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 498
DB 421 HSQWSPCSGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 480

QY 499 CPDAASTCTLWCTGTSGVLVVCOTKHPFPAWADGTSCEGKWCINGKCNKXNRKHFDT 558
DB 481 CPDAASTCTLWCTGTSGVLVVCOTKHPFPAWADGTSCEGKWCINGKCNKXNRKHFDT 540

Db 481 CPDAASTCTLWCTGTSGVLVCTQKHFPWADGTSCEGKWCINGKCNKTHKHFDTF 540
Qy 559 HGSWGMWPGWDCSRTCGGVQYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNNG 618
Db 541 HGSWGMWPGWDCSRTCGGVQYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNNG 600
Qy 619 KTFREEQCEAHNEFSKASFGSPAVIEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 678
Db 601 KTFREEQCEAHNEFSKASFGSPAVIEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 660
Qy 679 DGTSPSPDSTSVQVQCCVQKAGCDRIIDSKKKFDKCGVCGNGSTCKKISGVSATKPGY 738
Db 661 DGTSPSPDSTSVQVQCCVQKAGCDRIIDSKKKFDKCGVCGNGSTCKKISGVSATKPGY 720
Qy 739 HDIITPTGATNIEVKQNRNGSNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 798
Db 721 HDIITPTGATNIEVKQNRNGSNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 780
Qy 799 LRYSGSSAALIRISFSPLEPLTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSAM 858
Db 781 LRYSGSSAALIRISFSPLEPLTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSAM 840
Qy 859 VIEWGECSKSELGQWRRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEWS 918
Db 841 VIEWGECSKSELGQWRRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEWS 900
Qy 919 SCSKTCGKYKTSKLCLSHDGVLSHSDCLPKPKHFIDFCTMAECS 967
Db 901 SCSKTCGKYKTSKLCLSHDGVLSHSDCLPKPKHFIDFCTMAECS 949

RESULT 12

US-10-741-600-1605
; Sequence 1605, Application US/10741600
; Publication No. US2005026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1605
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1605

Query Match 97.1%; Score 5136; DB 17; Length 950;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 939; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 18 MGNARAPGSRGPGVPTLLALLAALLAVSDALGRPSEDEELVPELERVPGHGTTLR 77
Db 1 MGNARAPGSRGPGVPTLLALLAALLAVSDALGRPSEDEELVPELERVPGHGTTLR 60
Qy 78 LHAFDQDLDPDPSFLAPGFTLQNVGRKSGSDTLPETDLAHCFYSGTVNGDPSSAA 137
Db 61 LHAFDQDLDPDPSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSGTVNGDPSSAA 120
Qy 138 ALSICGVRGAFVLLGEAYFIQPLPAASERLATAAPEKPPAPLOHLLRRNEQDVGGT 197
Db 121 ALSICGVRGAFVLLGEAYFIQPLPAASERLATAAPEKPPAPLOHLLRRNEQDVGGT 180
Qy 198 CGVVDDPRPTGKAETDEDEGTGEGEPQWPDALQGVQPTGTGIRKKRVFSH 257
Db 181 CGVVDDPRPTGKAETDEDEGTGEGEPQWPDALQGVQPTGTGIRKKRVFSH 240
Qy 258 RYVETMLVADQSMAEFHGSLKHYLLTFLFVAARLYKHPISIRNSVSLVVKILVIHDEQK 317
Db 241 RYVETMLVADQSMAEFHGSLKHYLLTFLFVAARLYKHPISIRNSVSLVVKILVIHDEQK 300

Qy 318 GPEVTSNAALTILNFCNWKQHNPPSDRDAEHYDTAILFTTRQDLCSQTCDTILGMADVGT 377
Db 301 GPEVTSNAALTILNFCNWKQHNPPSDRDAEHYDTAILFTTRQDLCSQTCDTILGMADVGT 360
Qy 378 VCDPERSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKOCASLNGVNDQSHMMASLNL 437
Db 361 VCDPERSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKOCASLNGVNDQSHMMASLNL 420
Qy 438 DHSQWSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYDANRQCOTTFGEDSK 497
Db 421 DHSQWSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYDANRQCOTTFGEDSK 480
Qy 498 HCPDAASTCTLWCTGTSGVLVCTQKHFPWADGTSCEGKWCINGKCNKTHKHFDTF 557
Db 481 HCPDAASTCTLWCTGTSGVLVCTQKHFPWADGTSCEGKWCINGKCNKTHKHFDTF 540
Qy 558 FHSGWGMWPGWDCSRTCGGVQYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNN 617
Db 541 FHSGWGMWPGWDCSRTCGGVQYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNN 600
Qy 618 GKTFRREOCEAHNEFSKASFGSPAVIEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 677
Db 601 GKTFRREOCEAHNEFSKASFGSPAVIEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 660
Qy 678 VDGTPSPDSTSVQVQCCVQKAGCDRIIDSKKKFDKCGVCGNGSTCKKISGVSATKPG 737
Db 661 VDGTPSPDSTSVQVQCCVQKAGCDRIIDSKKKFDKCGVCGNGSTCKKISGVSATKPG 720
Qy 738 YHDIITPTGATNIEVKQNRNGSNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 797
Db 721 YHDIITPTGATNIEVKQNRNGSNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 780
Qy 798 VLRYSGSSAALIRISFSPLEPLTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSA 857
Db 781 VLRYSGSSAALIRISFSPLEPLTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSA 840
Qy 858 WIEWGECSKSELGQWRRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEW 917
Db 841 WIEWGECSKSELGQWRRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEW 900
Qy 918 SCSKTCGKYKTSKLCLSHDGVLSHSDCLPKPKHFIDFCTMAECS 967
Db 901 SCSKTCGKYKTSKLCLSHDGVLSHSDCLPKPKHFIDFCTMAECS 950

RESULT 13

US-09-741-151-4
; Sequence 4, Application US/09741151
; Publication No. US20020086400A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, Shiaooping et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001005
; CURRENT APPLICATION NUMBER: US/09/741,151
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Human
US-09-741-151-4

Query Match 95.3%; Score 5036; DB 9; Length 931;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 920; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 36 LLLAALLAVSDALGRPSEDEELVPELERVPGHGTTLRLHAFDQDLDPDPSF 95
Db 1 LLLAALLAVSDALGRPSEDEELVPELERVPGHGTTLRLHAFDQDLDPDPSF 60

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QY 96 LAPGFTLQVGRKSGSDTLPETDLAHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEA 155
DB 61 LAPGFTLQVGRKSGSETPLPETDLAHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEA 120
QY 156 YFIQPLPAASERLATAAPEGKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETED 215
DB 121 YFIQPLPAASERLATAAPEGKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETED 180
QY 216 EDEGTEGEDEGPQSPQDPALQGVGQPTGTGTSIRKKRFVSSHRYVETMLVADQSMAPFHG 275
DB 181 EDEGTEGEDEGAQSPQDPALQGVGQPTGTGTSIRKKRFVSSHRYVETMLVADQSMAPFHG 240
QY 276 SGLKHYLLTLFSVAARLYKHPSIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNW 335
DB 241 SGLKHYLLTLFSVAARLYKHPSIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNW 300
QY 336 QKQHNPPSDRDAEHYDVTAILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQA 395
DB 301 QKQHNPPSDRDAEHYDVTAILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQA 360
QY 396 AFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMMASMLSNLDHSPQSPSCGYMITSFL 455
DB 361 AFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMMASMLSNLDHSPQSPSCGYMITSFL 420
QY 456 DNGHGECLMDKQPNFIQLPDLPGTSYDANROQCTFGEDSKHCPDAASTCTLWCTGTS 515
DB 421 DNGHGECLMDKQPNFIQLPDLPGTSYDANROQCTFGEDSKHCPDAASTCTLWCTGTS 480
QY 516 GGVLVQCTKHFPWADGTSCEGKWCINGKCNKHKHFDTPFHGSGWGMWPGWDCSRTC 575
DB 481 GGVLVQCTKHFPWADGTSCEGKWCINGKCNKHKHFDTPFHGSGWGMWPGWDCSRTC 540
QY 576 GGGVQYTWRECDNVPVKGKGYCEGKRVYRSCNLEDCPDNNGKTFREBQCEAHNEFSA 635
DB 541 GGGVQYTWRECDNVPVKGKGYCEGKRVYRSCNLEDCPDNNGKTFREBQCEAHNEFSA 600
QY 636 SFGSGPAVEWIPKYAGVSPKDRCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCVQGO 695
DB 601 SFGSGPAVEWIPKYAGVSPKDRCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCVQGO 660
QY 696 CVKAGCDRIIDSKKFKDGVCGNGSTCKKISGTSVSAKPGYHDIITPTGATNIEVKQ 755
DB 661 CVKAGCDRIIDSKKFKDGVCGNGSTCKKISGTSVSAKPGYHDIITPTGATNIEVKQ 720
QY 756 RNQGRSNGSFLAIIKAADGTYILNGDYTLSTLEQDIMYKGVVLYRSGSSAALIRISFS 815
DB 721 RNQGRSNGSFLAIIKAADGTYILNGDYTLSTLEQDIMYKGVVLYRSGSSAALIRISFS 780
QY 816 PLKEBLTIQVLTVGNALRPKIYTVFKKKESFNAIPTFSAWVIEEWGECSKSCELGWQ 875
DB 781 PLKEBLTIQVLTVGNALRPKIYTVFKKKESFNAIPTFSAWVIEEWGECSKSCELGWQ 840
QY 876 RRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEMSSCKTCGKYKKTSLKC 935
DB 841 RRLVECRDINGOPASECAKEVPASTRPCADHPCPQWOLGEMSSCKTCGKYKKTSLKC 900
QY 936 LSHDGGVLSHSDCDPLKPKHPIDFCTMAEC 966
DB 901 LSHDGGVLSHSDCDPLKPKHPIDFCTMAEC 931
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RESULT 14
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; Sequence 7, Application US/10163316
; Publication No. US20020197703A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: A Human Matrix Metalloproteinase and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MPI01-025PIRNM
; CURRENT APPLICATION NUMBER: US/10/163,316
; CURRENT FILING DATE: 2002-06-05

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; PRIOR APPLICATION NUMBER: 60/297,863  
; PRIOR FILING DATE: 2001-06-13  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-163-316-7
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Query Match 81.2%; Score 4293.5; DB 13; Length 968;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 790; Conservative 58; Mismatches 112; Indels 15; Gaps 5;

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DB 1 MQRVPLGSRKQPCSDMGVDQRAARSRGSLSAHMLLLLASITMLLCARGAHGRTBED 60
QY 58 EELVPELERVPGHG--TTRLRLHAFDOQLDLDVDPDSFLAPGFTLQNVGRKSGSDTPL 115
DB 61 EELVPLSERAPGHDSITTRLRLDAFCQQLHLKLPDPSGFLAPGFTLQTVGRSPGSEAH 120
QY 116 --PETDLAHCYFSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLP-AASERLATAA 172
DB 121 LDPTGDLAHCYFSGTVNGDPGSAALSLCEGVGAFYLLQGBEFFIQAPAGVATERLAPAV 180
QY 173 PGEKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETEDDEGEDEGEDEGPQSPQ 232
DB 181 PEEESARPPQPHLLRRRRGGGAKCGVMDDETLP-----SDSRPESQNRNQMVPVR 233
QY 233 DPALQGVGQPTGTGTSIRKKRFVSSHRYVETMLVADQSMAPFHGSLKHYLLTLFSVAARL 292
DB 234 DPTPDACKPGSPGSGIRKKRFVSSPRYVETMLVADQSMADFHGSLGKHYLLTLFSVAARF 293
QY 293 YKHPISIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNWQKHNPSPSDRDAEHYDT 352
DB 294 YKHPISIRNSISLVVVKILVIYEEQKGPVTSNAALTILNFCNWQKHNSPSDRDPEHYDT 353
QY 353 ALLFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHD 412
DB 354 ALLFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHD 413
QY 413 DAKQACASLNGVNDQSHMMASMLSNLDHSPQSPSCGYMITSFLDNGHGECLMDKQPNFIK 472
DB 414 DAKHCKASLNGVTGDSHLMASMLSSLDHSPQSPSCSAYVWVTSFLDNGHGECLMDKQPNFIK 473
QY 473 LPDGLPGTSYDANROQCTFGEDSKHCPDAASTCTLWCTGTSGGVLVQCTKHFPWADGT 532
DB 474 LPDGLPGTLYDANROQCTFGEDSKHCPDAASTCTLWCTGTSGGVLLVCQTKHFPWADGT 533
QY 533 SCGEGKWCINGKCNKHKHFDTPFHGSGWGMWPGWDCSRTC CGGVGVYTMRECDNVPVK 592
DB 534 SCGEGKWCINGKCNKHKHFDTPFHGSGWGMWPGWDCSRTC CGGVGVYTMRECDNVPVK 593
QY 593 NGGKYCEGKRVYRSCNLEDCPDNNGKTFREBQCEAHNEFSAKSGSPGPAVEWIPKYAGV 652
DB 594 NGGKYCEGKRVYRSCNLEDCPDNNGKTFREBQCEAHNEFSAKSGNEFTVWTPKYAGV 653
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DB 774 ADGTYILNGDYTLSTLEQDIMYKGVVLYRSGSSAALIRISFSPLKEPLTIQVLTVGNAL 833
QY 833 RPKIKYTYTVFKKKESFNAIPTFSAWVIEEWGECSKSCELGHQRLVECRDINGOPASEC 892
DB 834 RPKIKYTYTVFKKKESFNAIPTFSEWVIEEWGECSKSCGSGWQRRVVQCRDINGHPASEC 893
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5232	99.0	967	4	US-09-130-491-2
2	5140	97.2	949	4	US-09-568-559-2
3	4260.5	80.6	950	4	US-09-321-987B-4
4	3922	74.2	727	4	US-09-445-023A-1
5	3656	69.2	727	4	US-09-445-023A-12
6	3297	62.4	608	4	US-09-130-491-13
7	2794	52.8	551	4	US-09-130-491-16
8	2471.5	46.7	950	4	US-10-009-332-1
9	2265.5	42.9	905	3	US-09-369-364A-9
10	2124	40.2	837	4	US-09-122-126B-2
11	2124	40.2	837	4	US-09-634-286A-2
12	2124	40.2	837	4	US-10-247-685-2
13	1924	36.4	930	4	US-09-122-126B-15
14	1924	36.4	930	4	US-09-634-286A-15
15	1924	36.4	930	4	US-10-247-685-15
16	1909.5	36.1	930	3	US-09-369-364A-2
17	1731.5	32.8	1882	3	US-09-369-364A-13
18	1608.5	30.4	2150	4	US-09-321-987B-2
19	1605.5	30.4	874	3	US-09-369-364A-15
20	1598	30.2	2165	4	US-09-800-729-155
21	1390.5	26.3	481	4	US-09-130-491-8
22	1293	24.5	518	3	US-09-369-364A-22
23	1287	24.3	1104	4	US-09-981-953A-4
24	1278.5	24.2	1224	4	US-09-930-872-4
25	1278.5	24.2	1224	4	US-10-217-774-4
26	1214.5	23.0	908	4	US-09-963-791-2
27	1207.5	22.8	997	3	US-09-369-364A-7

28	1176	22.2	1081	3	US-09-369-364A-17	Sequence 17, Appl
29	1151.5	21.8	757	4	US-09-963-791-24	Sequence 24, Appl
30	1100.5	20.8	1211	4	US-09-949-016-11401	Sequence 11401, A
31	1096	20.7	969	4	US-09-321-987B-5	Sequence 5, Appl
32	1083.5	20.5	1211	4	US-09-491-522-5	Sequence 5, Appl
33	1059	20.0	1205	4	US-09-491-522-11	Sequence 11, Appl
34	1029.5	19.5	859	3	US-09-369-364A-5	Sequence 5, Appl
35	1017	19.2	770	4	US-09-981-953A-2	Sequence 2, Appl
36	1001	18.9	1039	4	US-09-949-016-7859	Sequence 7859, Ap
37	781	14.8	589	4	US-09-963-791-12	Sequence 12, Appl
38	718	13.6	438	4	US-09-963-791-22	Sequence 22, Appl
39	712.5	13.5	245	3	US-09-369-364A-11	Sequence 11, Appl
40	595	11.3	1745	4	US-09-800-729-89	Sequence 89, Appl
41	593.5	11.2	507	4	US-09-963-791-10	Sequence 10, Appl
42	568.5	10.8	525	3	US-09-369-364A-21	Sequence 21, Appl
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44	566.5	10.7	845	4	US-09-784-358-12	Sequence 12, Appl
45	566.5	10.7	1691	4	US-09-784-358-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-130-491-2
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-491-2

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Qy	61	VPELERSVPGHGTTRLRLHAFDQDLDPDSSFLAPGTTLQNVGRKSGSDTLPETDL	120				
Db	61	VPELERSVPGHGTTRLRLHAFDQDLDPDSSFLAPGTTLQNVGRKSGSETLPETDL	120				
Qy	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180				
Db	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180				
Qy	181	LQFHLLRRNQDVGVTGCGVVDDEPRPTGKAETDEDEGTGEGDEGQWSPQDPALQGVG	240				
Db	181	LQFHLLRRNQDVGVTGCGVVDDEPRPTGKAETDEDEGTGEGDEGQWSPQDPALQGVG	240				
Qy	241	QPTGTGSIKRRFVSSHRYVETMLVADQSMAEFHGSLGHKHYLLTLPVVAARLYKHPISRN	300				
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Qy	301	SVSLVWVKILVIHDEQKGPVTSNAALTFRNFCNWKQKHNPPSDRDAEHYDTAILFTROD	360				
Db	301	SVSLVWVKILVIHDEQKGPVTSNAALTFRNFCNWKQKHNPPSDRDAEHYDTAILFTROD	360				

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DB 361 LCGSQTCDLGMADYCTVCDPSRSCSVIEDDGLQAAFTTAHGLGHVFNPHDPAKQACSL 420
QY 421 NGVNODSHMWSMLNLSHQSPWPCSGYMTSFLDNHGECLMDKPNQPIQLPGDLPGT 480
DB 421 NGVNODSHMWSMLNLSHQSPWPCSAYMTSFLDNHGECLMDKPNQPIQLPGDLPGT 480
QY 481 SYDANRQCFTTGEBSKHCPCDAASTCTLWCTGTSGVLVCTQKHPFPAWADGTSCEGKWC 540
DB 481 SYDANRQCFTTGEBSKHCPCDAASTCTLWCTGTSGVLVCTQKHPFPAWADGTSCEGKWC 540
QY 541 INKCKVNKHREFTPHGSGWMPGDCSRTCGGVQYTMRECDNPVPKNGKCYEG 600
DB 541 INKCKVNKTRKHFTPHGSGWMPGDCSRTCGGVQYTMRECDNPVPKNGKCYEG 600
QY 601 KRVYRSCNLEDCPNNGKTFREEQEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKL 660
DB 601 KRVYRSCNLEDCPNNGKTFREEQEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKL 660
QY 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSCKKFKDKCGVCGN 720
DB 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSCKKFKDKCGVCGN 720
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QY 781 GDTLSTLEQDIWYKGVLRYSGSSAALRIERSFPLKEPLTIQVLTGVALRPKIKYTY 840
DB 781 GDTLSTLEQDIWYKGVLRYSGSSAALRIERSFPLKEPLTIQVLTGVALRPKIKYTY 840
QY 841 FVKKKESFNAIPTSAWVIEBWGECSCSELGWQRRLVECRDINGQPASECAKEVKPAS 900
DB 841 FVKKKESFNAIPTSAWVIEBWGECSCSELGWQRRLVECRDINGQPASECAKEVKPAS 900
QY 901 TPCADHPCQOLGEWSSCKTCGKYKTSIKCLSHDGGVLSHDSCDPLKPKHFDIF 960
DB 901 TPCADHPCQOLGEWSSCKTCGKYKTSIKCLSHDGGVLSHDSCDPLKPKHFDIF 960
QY 961 CTMAECS 967
DB 961 CTMAECS 967

RESULT 2

US-09-568-559-2
; Sequence 2, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggreganase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-09-568-559-2

Query Match 97.2%; Score 5140; DB 4; Length 949;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 939; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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QY 79 HAFDOQLDLVPPDSSFLAPGFTLQNVGRKSGSDPLPETDLAHCFYSGTVNGDPSSAAA 138
DB 61 HAFDOQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLETDLAHCFYSGTVNGDPSSAAA 120
QY 139 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGKPPAPLOPHLLRRNRQGVGGTC 198
DB 121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGKPPAPLOPHLLRRNRQGVGGTC 180
QY 199 GVVDDEPRTKAEFTDEDECTEGEGEPQSPQDPAQGVGQPTGTGSIKRRFVSSH 258
DB 181 GVVDDEPRTKAEFTDEDECTEGEGEPQSPQDPAQGVGQPTGTGSIKRRFVSSH 240
QY 259 YVETMLVADQSMABPHGSLKHYLLTLFSAARLYKHPISIRNSVSLVVKILVHDEQKG 318
DB 241 YVETMLVADQSMABPHGSLKHYLLTLFSAARLYKHPISIRNSVSLVVKILVHDEQKG 300
QY 319 PEVTSNAALTUNFCNWOKQHNPPSDRDAEHYDTAILPTRQDLCSQTCDTLGMADVGT 378
DB 301 PEVTSNAALTUNFCNWOKQHNPPSDRDAEHYDTAILPTRQDLCSQTCDTLGMADVGT 360
QY 379 CDPSRSCSVIEDDGLQAAFTTAHGLGHVFNPHDPAKQACSLNGVNODSHMWSMLNLD 438
DB 361 CDPSRSCSVIEDDGLQAAFTTAHGLGHVFNPHDPAKQACSLNGVNODSHMWSMLNLD 420
QY 439 HSQWSPSCGYMTSFLDNHGECLMDKPNQPIQLPGDLPGTSYDANRQCQFTFGEDSKH 498
DB 421 HSQWSPSCGYMTSFLDNHGECLMDKPNQPIQLPGDLPGTSYDANRQCQFTFGEDSKH 480
QY 499 CPDAASTCTLWCTGTSGVIVCQKHPFPAWADGTSCEGKWCINGKCNVKNHKKHFDTPF 558
DB 481 CPDAASTCTLWCTGTSGVIVCQKHPFPAWADGTSCEGKWCINGKCNVKNHKKHFDTPF 540
QY 559 HGSWGMGPMGDCSRTCGGVQYTMRECDNPVPKNGKCYEGKRVYRSCNLEDCPDNNG 618
DB 541 HGSWGMGPMGDCSRTCGGVQYTMRECDNPVPKNGKCYEGKRVYRSCNLEDCPDNNG 600
QY 619 KTFREEQEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFFVLQPKV 678
DB 601 KTFREEQEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFFVLQPKV 660
QY 679 DGTCPSPDSTSVQVQCVKAGCDRIIDSCKKFKDKCGVCGNGSTCKKISGVTSAKPGY 738
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QY 739 HDIITPTGATNIEVKQNRGSRNNGSFLAIAKADGTYILNGDYLSTLEQDIWYKGV 798
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DB 781 LRYSGSSAALRIERSFPLKEPLTIQVLTGVALRPKIKYTYFVKKKESFNAIPTFSAW 840
QY 859 VIEWGECSKSELGWQRRLVECRDINGQPASECAKEVKPASTRCPADHPCQWOLGEWS 918
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DB 901 SCSTCKGKYKTSIKCLSHDGGVLSHDSCDPLKPKHFDIFCTMAECS 949

RESULT 3

US-09-321-987B-4
; Sequence 4, Application US/09321987B
; Patent No. 6730820
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bleiloch, Robert H

TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386
CURRENT APPLICATION NUMBER: US/09/321,987B
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/129,023
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 950
TYPE: PRT
ORGANISM: Murine
US-09-321-987B-4

Query Match 80.6%; Score 4260.5; DB 4; Length 950;
Best Local Similarity 81.8%; Pred. No. 0;
Matches 781; Conservative 56; Mismatches 105; Indels 15; Gaps 5;

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QY 73 TTRLRHLAFDQQLDLVPPDSFLAPFTLQNVKRGSGDTPL--PETDLAHCFYSGTVN 130
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DB 121 GDPGSAALSLCGRVGAFYLOGEFFIQPAGVATERLAPAPVEBESSARPOFHILRR 180
QY 190 RQGDVGTCGVVDEPRPTCKAETDEDETEGEGSPQSDPALQGVQPTGTGSGIR 249
DB 181 RRGSGAKGVMDETLPT-----SDSRPESQNTNQMPVRDPTPDQAGKSGFGSGIR 233
QY 250 KKEFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVSAARLYKHPISIRNSVSLVVKI 309
DB 234 KKEFVSSPRVYVETMLVADQSMADFHGSLGKHYLLTLFVSAARLYKHPISIRNSVSLVVKI 293
QY 310 LVTHDSQKGPVTSNAALTLRNFCNWKQKQNPSPDRDAEHYDTAILFTRODLGSGTCDT 369
DB 294 LVTYEKGKGPVTSNAALTLRNFCNWKQKQNPSPDRDPEHYDTAILFTRODLGSGTCDT 353
QY 370 LGMADVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKOCASLNGVNDQSHM 429
DB 354 LGMADVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCSLNGVTDGSHL 413
QY 430 MASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQCQ 489
DB 414 MASMLSLNLDHSPWSPCSAYMITSFLDNGHGECLMDKPNPIQLPSDLPGTLYDANRQCQ 473
QY 490 FTFGEBSKHCPDAASTCTLWCTGTSGGLVLCOTKHFPWADGTSCGEGKWCINGKVCNKN 549
DB 474 FTFGEBSKHCPDAASTCTLWCTGTSGGLVLCOTKHFPWADGTSCGEGKWCINGKVCNKT 533
QY 550 HRKHFTFPFHSGWGMWPGWDCSRTCGGGVQVYTMRECDNPVKNKGKVCSEKRVYRSCN 609
DB 534 DMKHFTFPFHSGWGMWPGWDCSRTCGGGVQVYTMRECDNPVKNKGKVCSEKRVYRSCN 593
QY 610 LEDCPDNNKGTFRREQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQOAKGI 669
DB 594 LEDCPDNNKGTFRREQCEAHNEFSKASFGNEPVEWIPKYAGVSPKDRCKLIQOAKGI 653
QY 670 FFVLQPKVDPGTPCSPDSTSVQVQGCVKAGCDRIIDSKKKFKCGVCGGNGSTCKKISG 729
DB 654 FFVLQPKVDPGTPCSPDSTSVQVQGCVKAGCDRIIDSKKKFKCGVCGGNGSTCKKMSG 713
QY 730 SVTSAPKGYHDLITIPGATNIEVKORNSRNGSFLAIKAADGYIILNGDYTLSTLE 789
DB 714 IVTSTREGYHDIIVIPAGATNIEVKHNRNSRNGSFLAIRAADGYIILNGDYTLSTLE 773
QY 790 QDIWKGVWLYRSGSSAALERIRSFSLKEPLTIQVLTGVNLRPKIKYTYFVKKKESF 849

DB 774 QDLTYKGTVLYRYSGSSAALERIRSFSLKEPLTIQVLTGVNLRPKIKYTYFVKKKTESF 833
QY 850 NAIPTFSAWVIBEWGECSCSCLGWORRLVECRDINGQPASECAKEVKVPASTRPCADHPC 909
DB 834 NAIPTFSEWVIBEWGECSCSKTCSGWORRVVQCRDINGHPASECAKEVKVPASTRPCADLPC 893
QY 910 POWQLGSEWSSCKTCGKYKTKSLKCLSHDGGVLSHSDCDPLKKPKHFIDFTMAEC 966
DB 894 PHWQGDWSPCSKTCGKYKTKLKVSHDGGVLSNESCDPLKKPKHYIDFCTLTQC 950

RESULT 4
US-09-445-023A-1
Sequence 1, Application US/09445023A
Patent No. 6565858
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Biiji
APPLICANT: Hakozaaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS-1
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 727
TYPE: PRT
ORGANISM: Homo sapiens
US-09-445-023A-1

Query Match 74.2%; Score 3922; DB 4; Length 727;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 707; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 248 IRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVSAARLYKHPISIRNSVSLVV 307
DB 8 LRKRFVSSPRVYVETMLVADQSMAEFHGSLGKHYLLTLFVSAARLYKHPISIRNSVSLVV 67
QY 308 KILVHDEQKGPVTSNAALTLRNFCNWKQKQNPSPDRDAEHYDTAILFTRODLGSGTQC 367
DB 68 KILVHDEQKGPVTSNAALTLRNFCNWKQKQNPSPDRDAEHYDTAILFTRODLGSGTQC 127
QY 368 DTLGMDVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKOCASLNGVNDQSD 427
DB 128 DTLGMDVGTVCDSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKOCASLNGVNDQSD 187
QY 428 HMWASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQ 487
DB 188 HMWASMLSLNLDHSPWSPCSAYMITSFLDNGHGECLMDKPNPIQLPGDLPGTLYDANRQ 247
QY 488 CQFTFGEDSKHCPDAASTCTLWCTGTSGGLVLCOTKHFPWADGTSCGEGKWCINGKVCN 547
DB 248 CQFTFGEDSKHCPDAASTCTLWCTGTSGGLVLCOTKHFPWADGTSCGEGKWCINGKVCN 307
QY 548 KNRKHFTFPFHSGWGMWPGWDCSRTCGGGVQVYTMRECDNPVKNKGKVCSEKRVYRYS 607
DB 308 KTDKHKHFTFPFHSGWGMWPGWDCSRTCGGGVQVYTMRECDNPVKNKGKVCSEKRVYRYS 367
QY 608 CNLEDCPDNNKGTFRREQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQOAKGI 667
DB 368 CNLEDCPDNNKGTFRREQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQOAKGI 427
QY 668 GYFVLPQKVPDGTGTPCSPDSTSVQVQGCVKAGCDRIIDSKKKFKCGVCGGNGSTCKKI 727

Db 428 GYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDKGCGVCGNGSTCKKI 487
QY 728 SGSVTSAGYVHDITITPGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLST 787
Db 488 SGSVTSAGYVHDITITPGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLST 547
QY 788 LQODIMYKGVLYRSGSSAALRIERSFSLKLEPLITQVLTGNALRPKIKYTYFVKKKKE 847
Db 548 LQODIMYKGVLYRSGSSAALRIERSFSLKLEPLITQVLTGNALRPKIKYTYFVKKKKE 607
QY 848 SFNAIPTSAWIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPASTRPCADH 907
Db 608 SFNAIPTSAWIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPASTRPCADH 667
QY 908 PCPQWLGWSSCKTCKGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFDIPTCMAECS 967
Db 668 PCPQWLGWSSCKTCKGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFDIPTCMAECS 727

RESULT 5
US-09-445-023A-12
; Sequence 12, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakezaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-445-023A-12

Query Match 69.2%; Score 3656; DB 4; Length 727;
Best Local Similarity 89.0%; Pred. No. 1.9e-311;
Matches 647; Conservative 42; Mismatches 38; Indels 0; Gaps 0;

QY 241 QPTGTGSTRKKKPVSSHRVETMLVADQSMAEFHGSLGKHYLLTLFSAARLYKHPISRN 300
Db 1 EPSGSGIRKKRFVSSPRVETMLVADQSMDFHSGSLGKHYLLTLFSAARLYKHPISRN 60
QY 301 SVSLVVKLVITHDEQKPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTROD 360
Db 61 SISLVVKLVITYEQKQPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTROD 120
QY 361 LCGSQTCDTLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSAL 420
Db 121 LCGSQTCDTLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSAL 180
QY 421 NGVNQDSHMAMSLNLDHSQWSPSCGYMITSFLDNHGECLMDKPNQPIQLPGDLPT 480
Db 181 NGVSGDHLAMSLNLDHSQWSPSCGYMITSFLDNHGECLMDKPNQPIQLPGDLPT 240
QY 481 SYDANRQCOFTFCEDSKHCPCDAASTCTLWCTGSGVLVVCOTKHPFPWADGTSCGEGKWC 540
Db 241 LYDANRQCOFTFCEDSKHCPCDAASTCTLWCTGSGVLVVCOTKHPFPWADGTSCGEGKWC 300
QY 541 INKGKCNKRNKHFDTFPFHGSGWGMGPWGDGCSRTCGGVQYTMRECDNPVPKNGGKYCBG 600
Db 301 VSGKCNKNTDMKHFATPVHSGSGWGMGPWGDGCSRTCGGVQYTMRECDNPVPKNGGKYCBG 360

QY 601 KVRVRSNLEDCPDNNGKTFREEOCEAHNBFPSKASFGSGPAVEWIPKYAGVSPKDRCKL 660
Db 361 KVRVRSNLEDCPDNNGKTFREEOCEAHNBFPSKASFGNEPTVETPKYAGVSPKDRCKL 420
QY 661 ICQAKIGIYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDKGCGVCGN 720
Db 421 TCEAKIGIYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDKGCGVCGN 480
QY 721 GSTCKKISGVSITSAKPGYHDITITPGATNIEVKORNGSRNNGSFLAIKAADGTIILN 780
Db 481 GSTCKKMSGIVTSTPGYHDITITPGATNIEVKORNGSRNNGSFLAIKAADGTIILN 540
QY 781 GDTLTSTLEQDIMYKGVLYRSGSSAALRIERSFSLKLEPLITQVLTGNALRPKIKYTY 840
Db 541 GNTLTSTLEQDITTYKGTVLYRSGSSAALRIERSFSLKLEPLITQVLMVGHALRPKIKYTY 600
QY 841 FVKKKESFNAIPTFSAWVIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPAS 900
Db 601 FMKKKTESFNAIPTFSAWVIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPAS 660
QY 901 TRPCADHPCPQWLGWSSCKTCKGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFDIPT 960
Db 661 TRPCADHPCPQWLGWSSCKTCKGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFDIPT 720
QY 961 CTMAECS 967
Db 721 CTLTQCS 727

RESULT 6
US-09-130-491-13
; Sequence 13, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-130-491-13

Query Match 62.4%; Score 3297; DB 4; Length 608;
Best Local Similarity 90.9%; Pred. No. 4.3e-280;
Matches 599; Conservative 1; Mismatches 5; Indels 54; Gaps 1;

QY 309 ILVIHDEQKPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRODLCGSQTC 368
Db 4 ILVIHDEQKPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRODLCGSQTC 63
QY 369 TLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSALNGVQDSH 428
Db 64 TLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSALNGVQDSH 123
QY 429 WMAASMLNLDHSQWSPSCGYMITSFLDNHGECLMDKPNQPIQLPGDLPGTSDANROC 488
Db 124 WMAASMLNLDHSQWSPSCGYMITSFLDNHGECLMDKPNQPIQLPGDLPGTSDANROC 183
QY 489 OPTFCEDSKHCPCDAASTCTLWCTGSGVLVVCOTKHPFPWADGTSCGEGKWCINGKCNK 548
Db 184 OPTFCEDSKHCPCDAASTCTLWCTGSGVLVVCOTKHPFPWADGTSCGEGKWCINGKCNK 243

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QY 549 NHRKHEDTPPHGSMWGMWGDSCRTCCGGVQVYTMRECDNVPVKNKGKCEGRVYRSC 608
Db 244 TDRKHEDTPPHGSMWGMWGDSCRTCCGGVQVYTMRECDNVPVKNKGKCEGRVYRSC 303
QY 609 NLEDCPDNNGKTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKORCKLIQAKGIG 668
Db 304 NLEDCPDNNGKTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKORCKLIQAKGIG 363
QY 669 YFVLQPKVVDGTPCSPDSTSVCCQGVKAGCDRIIDSKKFKDKGVCNGNSTCKKLS 728
Db 364 YFVLQPKVVDGTPCSPDSTSVCCQGVKAGCDRIIDSKKFKDKGVCNGNSTCKKLS 423
QY 729 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 788
Db 424 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 483
QY 789 EQDIMYKGVVLYRYSGSAALERIRSFPLKEPTIQVLTGVNLRPKIKYTFVKKKKB 848
Db 484 EQDIMYKGVVLYRYSGSAALERIRSFPLKEPTIQVLTGVNLRPKIKYTFVKKKKB 543
QY 849 FNAIPTFSAWIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEVKPASTPCADHP 908
Db 544 FNAIPTFSAWIEBWGE----- 560
QY 909 CPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDIDFCTMAECS 967
Db 561 -----CSKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDIDFCTMAECS 608

RESULT 7
US-09-130-491-16
; Sequence 16, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; PRIOR FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 551
; ORGANISM: Rattus rattus
US-09-130-491-16

Query Match 52.8%; Score 2794; DB 4; Length 551;
Best Local Similarity 88.0%; Pred. No. 4,7e-236;
Matches 485; Conservative 35; Mismatches 31; Indels 0; Gaps 0;

QY 417 CASLNGVNDSHMWSMLSLDHSQWSPSCGYMTSFLNGHGECLMDKQPNQIQLPGD 476
Db 1 CASLNGVSGDLSHMLSLDHSQWSPSCGYMTSFLNGHGECLMDKQPNQIQLPSD 60
QY 477 LPGTSYDANRQCQTFEGEDSKHCPDAASTCTLWCTGTSGGLVVCQTKHPFWDGTSCE 536
Db 61 LPGTLYDANRQCQTFEGESKHCPDAASTCTLWCTGTSGGLVVCQTKHPFWDGTSCE 120
QY 537 GKWCINGKCVKNHRKHFDTPPHGSMWGMWGDSCRTCCGGVQVYTMRECDNVPVKNKGK 596
Db 121 GKWCVSGKCVKNKTDKMHFATPHVSGWGPWGDSCRTCCGGVQVYTMRECDNVPVKNKGK 180
QY 597 YCEGRVYRYSKULEDCPDNNGKTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKD 656
Db 181 YCEGRVYRYSKNTEDCPDNNNGKTFRBQCEAHNEFSKASFGNEPTVETWTPKYAGVSPKD 240
QY 657 RCKLIQAKGIGYFFVLQPKVVDGTPCSPDSTSVCCQGVKAGCDRIIDSKKFKDKGCV 716
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Db 241 RCKLIQAKGIGYFFVLQPKVVDGTPCSPDSTSVCCQGVKAGCDRIIDSKKFKDKGCV 300
QY 717 CGNGSTCKKISGSVTSKAPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 776
Db 301 CGNGSTCKKMSGIVTSTPRGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 360
QY 777 YILNGDYTLSTLQDITMYKGVVLYRYSGSAALERIRSFPLKEPTIQVLTGVNLRPKI 836
Db 361 YILNGDYTLSTLQDITMYKGVVLYRYSGSAALERIRSFPLKEPTIQVLTGVNLRPKI 420
QY 837 KYTFYVKKKKBSPNAIPTFSAWIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 896
Db 421 KYTFYVKKKKBSPNAIPTFSAWIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 480
QY 897 KPASTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKKH 956
Db 481 KPASTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKKH 540
QY 957 FIDFCTMAECS 967
Db 541 YIDFCTMAECS 551

RESULT 8
US-10-009-332-1
; Sequence 1, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGRECANASE ACTIVITY
; FILE REFERENCE: 067541
; CURRENT APPLICATION NUMBER: US/10/009,332
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 950
; ORGANISM: Homo sapiens
US-10-009-332-1

Query Match 46.7%; Score 2471.5; DB 4; Length 950;
Best Local Similarity 48.0%; Pred. No. 2.1e-207;
Matches 484; Conservative 153; Mismatches 253; Indels 101; Gaps 24;

QY 36 LILALAAALLAVSDALGRPSEDESELYVP-ELE-----RVP---GHGTTLRRLHAF 81
Db 1 MLLGLILTLTAFAGRTAGGFEPREVVPVIRLDDPDINGRRYRWKGPESDQGLIFITAP 60
QY 82 DQQLDLDPDPSFLAPGFTLQNVGRKSGSDTLP-----ETDLAHCFYSGTVNGDPSSA 136
Db 61 QEDFYHLTLTDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
QY 137 AALSCEGVKAGFVLLGEAYFIQPLPAASRLATAPEKPPAPLQFHLLRNQGVGG 196
Db 115 AAVSLCGLRGAFYRGAEYVISPPLNAS---APAAQRNSQGA---HLLQ---RRGVPGG 165
QY 197 TCGVDDDEPPTKAEETDEDEGTEDEGPQS-----PQDPALQGVGP-TGTGS 247
Db 166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGGESRRRS 207
QY 248 IRKRKFVSSHRYVETMLVADQSMAEFGSLKHYLLTLFSAARLYKHPSTRNVSLLVV 307
Db 208 GRKRKFVSIPIRYVETLVVADSVKFGADLEHYLLTLTAAARLYRHPSTLNINIVV 267
QY 308 KILVHDEQKGPVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTQDLCGSGTCC 367
Db 308 KILVHDEQKGPVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTQDLCGSGTCC 367
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Db 268 KVLRLDRDSGPKVTGNAALTLRNFCAWQKLNKYSKDHPEYWDTAILFTRODLGATTC 327
QY 368 DTLGMDVCTVCDPSRSCSVIEDDGLQAFTHAHELGHVFNPHDDAKOCASLNGVQDS 427
Db 328 DTLGMDVCTVCDPSRSCSVIEDDGLQAFTHAHELGHVFNPHDVKVCEVFGKLRAN 387
QY 428 HMASMLNLDHSPQWSPGSGYMIITSLDNGHGECLMDKPNPIOLPGDLPGTSDYANRQ 487
Db 388 HMASMLNLDHSPQWSPGSGYMIITSLDNGHGECLMDKPNPIOLPGDLPGTSDYANRQ 447
QY 488 COFTTEGSKHCPDAASTCTLWCTGTSGVILVQTKHPPWADGTSCEGKWCINGKCNV 547
Db 448 CELAFGVGSKPCP-YMQYCTKLWCTGKAGQWVCQTRHPPWADGTSCEGKCLKGACVE 506
QY 548 K-NHRKHFTPHGSGWMPGWDGSCRTSGGQVQYTMRECDNPPVNGGKYCEGKRVYR 606
Db 507 RHNLAKH---RVDSWAKWDPTGPCSRTCGGVQVQLARRQCTNPTTPANGGKYCEGKRVYR 563
QY 607 SCNLEDCPDN-NGKTFREOCEAHNEFSKASFGSGPAVEWI PKYAGVSPKDRCKLICQAK 665
Db 564 SCNLEDCPDN-NGKTFREOCEAHNEFSKASFGSGPAVEWI PKYAGVSPKDRCKLICQAK 623
QY 666 GTGYFVLQPKVVDGTPSPDSTVSCVQGCYKAGCDRIIDSKKXFKDGVCGGNGSTCK 725
Db 624 GTGYFVLQPKVVDGTPSPDSTVSCVQGCYKAGCDRIIDSKKXFKDGVCGGNGSTCK 683
QY 726 KISGVSNAKPGYHDIITPTGATNIEVKQNRQSRNNGSPFLAKAADGTIINGDYTL 785
Db 684 KVTGLFTPMHGYNFVVAIPAGASSIDIRQRYKGLIGDNYLALNKGKYLNGHFV 743
QY 786 STLEODIMYKGVVLYSGSSAALERSPSPLKEPLTIQVLTGVALRPKIKYTVFVKK 845
Db 744 SAVERDLVKGSLLYSGTGAVESLQASRPFILEPLTVEVLVSGKMTTPRVRYSYLPKE 803
QY 846 ---KES-----FNAIPTFS-----AWIEEGECSKSCELQWQRL 878
Db 804 PREDKSSHPKDPGRGSPVLHNSVLSNOVEQPDPRPARWAGSNWGPCSASCGSLQKRA 863
QY 879 VECRINO---PASECAKEVPASTRPCADHPCQWOLGEWSSCKYCKGKYSILKC 935
Db 864 VDCRSAGQRTVPACDAAH--RPVETOACGE-PCPTWELSAWSPSCSGRFGORRLK 920
QY 936 LSHDGVSHSDCDPLKPKPHIDFTMAEC 966
Db 921 VCHGSRLLARDQCNLHRKQOE-LDFCVLRPC 950

RESULT 9
US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Mus musculus ADAMTS-8
US-09-369-364A-9

Query Match 42.9%; Score 2265.5; DB 3; Length 905;
Best Local Similarity 47.9%; Pred. No. 2.2e-189;
Matches 441; Conservative 146; Mismatches 263; Indels 71; Gaps 18;
QY 34 PTLALLAALAVSDALGRPS-----EEDDELVPELERYVPGHGT-TRLRLHAFQQLDL 87

Db 11 PPLLLLLLQPPPLVCGAPAGPGTGAQASLAVP--TRLPGSASELAFLHSAFGQGFVL 68
QY 88 DVPPSSSLAFCFTLQNVGRKSGSDTLPETDLAHCFFYSGTVNGDPSSAAALSCEGVG 147
Db 69 RIAPDASFLAEPFKTERLIGGSSAAAG--GEPGLRCGCFSGTVNGERESLAAMSCVAGMSG 126
QY 148 AFYLLGEAYFYQPLPAAS-----ERLATAAPQCEK-----PAPLQFHLLRN 189
Db 127 SFLAGEFTTQPGAGSLDQPHRLQWGFQORREDPLAAAEVFPPLQGLEWEWEN 186
QY 190 RQGDVGGTGVVDDPRPTGKAETDEDETEGEDEGEQWSPQDPALQGVGQFTGTGIR 249
Db 187 GQGG-----ERSDNEEDKKQDKKGLKETEDS--AKVPPFPFGS-KTR 225
QY 250 KRFVSSHYRYVETMLVADQSMAEFGSGLKHVLLTLFSAARLYKHPSIRNSVLSVVKI 309
Db 226 SKRFVSEARFVETLLAVADASMAAFYGTDLQNHILTVMSMAARIYKHPSIRNSVLSVVKI 285
QY 310 LVIHDEQKGPVTSNAALTLRNFCAWQKLNKYSKDHPEYWDTAILFTRODLGATTC 368
Db 286 LIVEKRWGPEVSDNGGLTLRNFCSWQRRFKPSDRHPEHYDTAILFTROFCGKEQCD 345
QY 369 TLGMADVCTVCDPSRSCSVIEDDGLQAFTHAHELGHVFNPHDDAKOCASLNGVQDS 428
Db 346 TLGMADVCTVCDPSRSCSVIEDDGLQAFTHAHELGHVFNPHDDAKOCASLNGVQDS 405
QY 429 HMASMLNLDHSPQWSPGSGYMIITSLDNGHGECLMDKPNPIOLPGDLPG--TSYDANR 486
Db 406 MMAPPFIHVNKTLPMSPCSAVYLTLLDGHGDCLLDAPTSLPLPTGLPGHSTIYELDO 465
QY 487 OCQFTFGSDSKHCPDAA--STCSTLWCTGTSGVILVQTKH--FPWADGTSCEGKWCIN 542
Db 466 QCKQIFGDPFHCPNTSVEDICVQLCAHRSDEPICHTKNGSLWADGTPCGPHLCLD 525
QY 543 GKVNKXHKHFDTPFHGSGWMPGWDGSCRTSGGQVQYTMRECDNPPVNGGKYCEGKR 602
Db 526 GCVLKEDVENPKAVVDGWDGFWRPWQGCRTSGGQVQYTMRECDNPPVNGGKYCEGKR 585
QY 603 VYRSCNLEDPCDNNKGTFRBOCEAHNEFSKASFGSGPAVEWI PKYAGVSPKDRCKLIC 662
Db 586 VKYQSCNTEBEP--NGKSFREOCEAHNEFSKASFGSGPAVEWI PKYAGVSPKDRCKLIC 643
QY 663 OAKGIGYFVLQPKVVDGTPSPDSTVSCVQGCYKAGCDRIIDSKKXFKDGVCGGNGS 722
Db 644 RARGSEPKVPEAKVIDTLCGPDTLSCVRCQCVKAGCDHVVNSPKLDCGVCGRGT 703
QY 723 TCKKISGVSNAKPGYHDIITPTGATNIEVKQNRQSRNNGSPFLAKAADGTIINGDY 782
Db 704 ACRKISGVSNAKPGYHDIITPTGATNIEVKQNRQSRNNGSPFLAKAADGTIINGDY 763
QY 783 YTLSTLEODIMYKGVVLYSGSSAALERSPSPLKEPLTIQVLTGVALRPKIKYTVF 841
Db 764 LAISAIEDQILVKGTILKYSGMATLERLQSFALPEPLTVQLLTVSGVEFPKRYTYFF 823
QY 842 V-----KKKESFNAIPTF--SAWIEEGECSKSCELQWQRLVCECRDINGOPA 889
Db 824 VPNDMDPSVQNSKERATNIIQSLPSAEWVLGDWSECFSTCEGSWQRRTECEDPFGQAS 883
QY 890 SECAKEVPASTRPCADHPCP 910
Db 884 DTCDEALKPEDAKPCGQPCP 904

RESULT 10
US-09-122-126B-2
; Sequence 2, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGATE DEGRADING METALLO PROTEASES
; FILE REFERENCE: DMG909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24

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; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-122-126B-2

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Query Match 40.2%; Score 2124; DB 4; Length 837;
Best Local Similarity 49.0%; Pred. No. 5e-177;
Matches 411; Conservative 132; Mismatches 225; Indels 70; Gaps 18;

RESULT 11

RESULT II
US-09-634-286A-2

US-09-634-286A-2
: Sequence 2: Application US/09634286A

; sequence 2, Application No. 6521436

RESULT 12

US-10-247-685-2

; Sequence 2, Application US/10247685

; Patent No. 6753176

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909D

; CURRENT APPLICATION NUMBER: US/10/247,685

; CURRENT FILING DATE: 2002-09-19

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 837

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-247-685-2

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DB 97 EQDSGVQVEGLTVQLGAPELLGAE---PGT-----YLTGTINGDPESVASLHWDGGA 148
QY 145 VRGAFYLLGEAYFIQPLPAASERLATAAPGKPPAPLOPHLLRRNRQGDVGTCGVVDDE 204
DB 149 LLGVLYQYGAELHQLPLEGGTNSA--GGPGA-----HILRRK----- 184
QY 205 PRPTGKAETEDDETEGEDEGPQSPQDPALQGVGQGTGTSIRKRFVSSHRYVETML 264
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QY 265 VADQSMARFHSGLKHVLLTLFVSVAARLYKHPISIRNSVSLVVKLVTHDQKGEVTSN 324
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QY 504 STCSLTWCTGTSGGVLCVQTKHFPWADGTCGEGKWCINGKVCNKNRKHFDTPPHGSGW 563
DB 465 PPCAALWCSHUNGHAMCQTKHSPWADGTPCPAQACMGGRCLHMDQLQDFNIPQAGGW 524
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QY 624 EQCEAHNFEKASFGSGPA--VEWIPKYAGVSPKDRCKLIQAKGIGYFFVLQPKVVDGTP 682
DB 585 EQCAAYNHRDIL--FKSFPFGMDVPRYTGVAPODQCKLTQARALGYTVVLEPRVVDGTP 643
QY 683 CSPDSTSCVQOCVKAGCDRIIDSKKXFDKGVCGGNGSTCKLTSGSVTSKAPGYHDII 742
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QY 743 TIPTGATNIEVKQRNQRNNGNSFLAIKAADGTVILNGDVTLSLEQDIMYKGVV--LRY 801

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US-09-122-126B-15

; Sequence 15, Application US/09122126B

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122,126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 930

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-122-126B-15

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Best Local Similarity 40.7%; Pred. No. 2e-159;

Matches 391; Conservative 125; Mismatches 314; Indels 130; Gaps 17;

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GenCore version 5.1.6
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Run on: May 23, 2005, 19:02:38 ; Search time 1179 Seconds
(without alignments)

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Perfect score: 5287

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Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database :

Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	5287	100.0	4014	11	US-09-989-687-125	Sequence 125, Appl
2	5232	99.0	3430	18	US-10-473-974-98	Sequence 98, Appl
3	5232	99.0	4014	16	US-10-115-286-1	Sequence 1, Appl
4	5232	99.0	4014	18	US-10-757-450-1	Sequence 1, Appl
5	5232	99.0	4676	13	US-10-105-929-1	Sequence 1, Appl
6	5230	98.9	3889	19	US-10-667-281-1	Sequence 1, Appl
7	5224	98.8	4309	16	US-10-210-120-57	Sequence 57, Appl
8	5224	98.8	4447	18	US-10-753-889-133	Sequence 133, Appl
9	5224	98.8	4459	17	US-10-159-563-192	Sequence 192, Appl
10	5224	98.8	4459	17	US-10-159-563-308	Sequence 308, Appl
11	5224	98.8	4760	10	US-09-971-4298-17	Sequence 17, Appl
12	5202	98.4	4352	19	US-10-741-600-776	Sequence 776, Appl
13	5202	98.4	4459	19	US-10-741-600-777	Sequence 777, Appl
14	5202	98.4	4658	19	US-10-741-600-775	Sequence 775, Appl
15	5144	97.3	3261	10	US-09-373-658-1	Sequence 1, Appl
16	5144	97.3	3261	11	US-09-989-687-1	Sequence 1, Appl
17	5140.5	97.2	4848	17	US-10-425-114-26851	Sequence 26851, A
18	4302.5	81.4	21130	19	US-10-741-600-17789	Sequence 17789, A
19	4293.5	81.2	4858	19	US-10-764-420-37	Sequence 37, Appl
20	4287	81.1	4878	17	US-10-191-803-170	Sequence 170, Appl
21	4287	81.1	4878	17	US-10-152-319A-1840	Sequence 1840, App
22	4277.5	80.9	4180	10	US-09-373-658-20	Sequence 20, Appl
23	4277.5	80.9	4180	11	US-09-989-687-20	Sequence 20, Appl
24	4270.5	80.8	2871	18	US-10-473-974-23	Sequence 23, Appl
25	3922	74.2	2184	9	US-09-445-023A-2	Sequence 2, Appl
26	3922	74.2	2184	14	US-10-097-597-2	Sequence 2, Appl
27	3922	74.2	2184	14	US-10-097-580-2	Sequence 2, Appl
28	3652	69.1	2184	9	US-09-445-023A-13	Sequence 13, Appl
29	3652	69.1	2184	14	US-10-097-597-13	Sequence 13, Appl
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31	3411	64.5	9248	10	US-09-373-658-21	Sequence 21, Appl
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33	3303	62.5	3147	18	US-09-803-589-1	Sequence 1, Appl
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35	2642	50.0	3145	18	US-09-803-589-9	Sequence 9, Appl
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37	2498.5	47.3	2804	17	US-10-093-463-27	Sequence 27, Appl
38	2496	47.2	3446	9	US-09-965-631-7	Sequence 7, Appl
39	2496	47.2	3446	19	US-10-961-020-7	Sequence 24, Appl
40	2478.5	46.9	2937	17	US-10-275-107-24	Sequence 24, Appl
41	2478	46.9	2853	9	US-09-965-631-3	Sequence 3, Appl
42	2478	46.9	2853	18	US-10-391-364-76	Sequence 76, Appl
43	2478	46.9	2853	18	US-10-391-364-78	Sequence 78, Appl
44	2478	46.9	2853	19	US-10-753-267-55	Sequence 55, Appl
45	2478	46.9	2853	19	US-10-961-020-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)

OTHER INFORMATION:
US-09-989-687-125

Alignment Scores:

Pred. No.: 0 Length: 4014
Score: 5287.00 Matches: 967
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

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Db 2446 ATCTGCCAAGCCCAAGGCAATGGCTACTCTCTCTGTTTTCAGGCCCAAGGTTGTAGATGTT 2505
Qy ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValVallLeuAAGly 700
Db 2506 ACTCCATGATGAGCCCAATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGGT 2565
Qy CysAspArgIleleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2566 TGTGATCGCATCATAGACTCCAAAAGAGAGTTTGTATAAATGTGTGTTCGGGGGAAAT 2625
Qy GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyThrHisAsp 740
Db 2626 GGATCTACTTGTAAAAAATATCAGGATCAGTGTACTAGTGCAAAACCTGGATATCATGAT 2685
Qy IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2686 ATCATCACAAATTCACCTGAGGCCACCAACATCGAAGTGAACAGCGGAACAGAGGGA 2745
Qy SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrlleLeuAsn 780
Db 2746 TCCAGGAACAATGGCAGCTTCTTGCCATCAAGCTGCTGATGCGACATATATCTTAAT 2805
Qy GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValVallLeuArg 800
Db 2806 GGTGACTACACTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGAGG 2865
Qy TyrSerGlySerSerAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2866 TACAGCGGCTCTCTCGGCAATGGAAAGAAATTCGACAGCTTTAGCCCTCTCAAAAGGCC 2925
Qy LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2926 TTGACCATCCAGTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACTAC 2985
Qy PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2986 TTCTGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3045
Qy GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3046 GAAGAGTGGGGCGGAATGTTCTAAGTCAATGTGAATGGTGTGGCAGAGAAGCTGGTAGAA 3105
Qy CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TGCAGAGACATTAATGGACAGCTGCTTCCAGTGTGCAAGAGAGTGAAGCCAGCCAGC 3165
Qy ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCGAGTGGTCAATCATGT 3225
Qy SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3226 TCTAAGACCTGTGGAGGTTTCAAAAAAACAAGCTTGAAGTGTCTGTCCCAATGATGGA 3285
Qy GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGACAGCTGTGATCTTTAAGAAACCTTAAACATTTTCATAGACTTT 3345
Qy CysThrMetAlaGluCysSer 967
Db 3346 TGCACAAATGGCAGAAATGCAGT 3366

RESULT 2

US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US2004026580A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILLHABER, JOACHIM

; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Alignment Scores:
Pred. No.: 0 Length: 3430
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 18 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-473-974-98 (1-3430)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 187 ATGCAGCAGAGCTGTGCCCGAGGGGTTCGGAAGCGCAAGCTGGGACGACATCGGGAAAC 246
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 247 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCGGCTACCCACGCTGCTGTCTGCC 306
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 307 GCGGCGCTACTGGCCGTGTCCGACGCACCTCGGGCGCCCTCCGAGGAGGACGAGGACTA 366
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 367 GTGGTCCGGAGCTGGAGCGCGCCCGGGACACGGGACACGCGCTTCCGCTGCGACGCC 426
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 427 TTTGACACGACGCTGATCTGGAGCTGCGGCGCCGACAGCAGCTTTTGGCGCGCGCTTC 486
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 487 ACGCTCCAGAACGTGGGGCGCAAAATCCGGTCCGAGACGCGCTTCCGGAACCGACCTG 546
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 547 GCGCACTGCTTCTACTCCGCGACCCGGAATGGCGATCCCGAGCTCGGCTCGCGCCCTCAG 606
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 607 CTCTGAGGGCGTGGCGGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCG 666
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 667 CTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAAGCGCGCGCACCA 726
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 727 CTACAGTTCCACCTCTCTGGCGGGAATTCGACAGGCGACGTAAGCGCGCACGTGCGGGGTC 786

QY	201	ValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluAspGluGlyThr	220	QY	561	SerTyrGlyMetTyrProTyrProTyrGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	787	GTGGACGACGAGCCCGCGCGACTGGGAAGCGGAGACCGAAGACGAGGAGGACT	846	DB	1867	AGCTGGGAGATGTGGGGCTTGGGAGACTGTTGAGAACGTCGGTGGAGGATCCAG	1926
QY	221	GluGlyGluAspGluGlyProGlnTyrSerProGlnAspProAlaLeuGlnGlyValGly	240	QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyrCysGluGly	600
DB	847	GAGGGCGAGGACGAAGGGCTCAGTGGTCGCCGACGACCCGGCACTGCAAGGCGTAGGA	906	DB	1927	TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGC	1986
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260	QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnGlnLysThr	620
DB	907	CAGCCACACAGGAACGTGAAGACATAAGAAAGAACGATTTGTGTCCAGTCCACGCTATGTG	966	DB	1987	AAACCCAGTGGCTACAGATCCCTGTAACTTGGAGACTGTCCAGACAATATATGAAAAACC	2046
QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280	QY	621	PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640
DB	967	GAACCATGCTTGTGGCAGACCATCGATGGCAGAAATCCAGCGCAGTGGTCTAAGACAT	1026	DB	2047	TTTAGAGAGAACATGTGAGCACACACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGG	2106
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300	QY	641	ProAlaValGluTyrIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
DB	1027	TACCTTCTCAGTGTGTTTCGGTGGCAGCCAGATTGTACAAACCCACAGCATTCGTAT	1086	DB	2107	CCTGGGTGGATGGATTCCCAAGTAGCGTGGCTCTCACCAAGGACAGGTGCAAGCTC	2166
QY	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320	QY	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValAlaAspGly	680
DB	1087	TCAGTTAGCTGTGGTGTGAAGATCTTGTGTCATCCAGCATGACAGGAGCGCGAA	1146	DB	2167	ATCTCCCAAGCCAAAGGCATTGGCTACTTCTTCTGTTTGCAGCCCCAAGTTGTAGATGT	2226
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTyrGlnLysGlnHisAsn	340	QY	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
DB	1147	GTGACCTCAATGCTGCCCTCACTTCGCGAACTTTTGGAACTGGCAGAAAGCAGACAAC	1206	DB	2227	ACTCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGTGT	2286
QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360	QY	701	CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn	720
DB	1207	CAACCCAGTGACCGGATGCAGAGCACTATGACACAGCAATTTCTTTACACAGACGAC	1266	DB	2287	TGTGATCGCATCATAGACTCCAAAAAGAAAGTTGATAAATGTGGTGTTCGGGGGAAAT	2346
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380	QY	721	GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp	740
DB	1267	TTGTGTGGGTCCACAGATGTGATCTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT	1326	DB	2347	CGATCTACTTGTAAAAAATAATACGATCAGTTACTAGTGCAAAAACCTCGATATCATGT	2406
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400	QY	741	IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly	760
DB	1327	CCGAGCAGAAGCTGCTCCGCTCATAGAAAGATGATGTTTACAAGCTGCCCTTACACAGCC	1386	DB	2407	ATCATCACAAATTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAACAGAGGGA	2466
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420	QY	761	SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn	780
DB	1387	CATGAATTAGGCCACCGTGTAAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT	1446	DB	2467	TCAGAGAAACAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATATATTTCTAAT	2526
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440	QY	781	GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg	800
DB	1447	AATGGTGTGAACCGAGATTCCACATGATGGCGTCAATGCTTTCCAACCTGGACCAAGC	1506	DB	2527	GGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGACAAGGTGTTGTCTTGAGG	2586
QY	441	GlnProTyrSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460	QY	801	TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro	820
DB	1507	CAGCCTTGTCTCTTGGCAGTCCATCATGATTACATCATTTCTGGATTAATGTCATGGG	1566	DB	2587	TACAGCGGCTCTCTGGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGGCC	2646
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480	QY	821	LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr	840
DB	1567	GAATGTTTGTGACAAAGCTCAGAAATCCATACAGCTCCCGGCGATCTCCCTGGCACC	1626	DB	2647	TTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC	2706
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500	QY	841	PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle	860
DB	1627	TGCTAGCATGCCAACCGGAGTCCAGTTTACATTTTGGGGAGGACTCCAAACACATGCCCT	1686	DB	2707	TTTCGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTTCAGCATGGGTCAT	2766
QY	501	AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyValLeuVal	520	QY	861	GluGluTyrGlyGluCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGlu	880
DB	1687	GATGCAGCCAGACATGTAGACACTTGTGTGTATCCGCGACCTCTGTTGGTGGGTGTCTGGT	1746	DB	2767	GAAGAGTGGGCGAATGTTCTAAGTCAATGTAATGGGTGGCAGAGAAGACTGGTAGAA	2826
QY	521	CysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGlyLysTyrCys	540	QY	881	CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer	900
DB	1747	TGTCAAAACCAACACTTCCCGTGGGCGGATGACACAGCTGTGGAGAAAGGAAATGTTGT	1806	DB	2827	TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTGCAAGAGAAAGTGAAGCCAGCACG	2886
QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560	QY	901	ThrArgProCysAlaAspHisProCysProGlnTyrGlnLeuGlyGluTyrSerSerCys	920
DB	1807	ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGTATACGCTTTTTCATGGA	1866	DB	2887	ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGCAGCTCGGGAGTGGTCACTCATGT	2946
				QY	921	SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly	940

Db 2947 TCTAAGACCTGTGGGAGGGTTACAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGA 3006
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuIysProIysHisPheIleAspPhe 960
Db 3007 GGGGTGTATCTCATGAGAGCTGTGATCTCTTAAGAAACCTAAACATTTTCATAGACTTT 3066
Qy 961 CysThrMetAlaGluCysSer 967
Db 3067 TGCACAAATGGCAGATGCAGT 3087

RESULT 3

US-10-115-286-1
; Sequence 1, Application US/10115286
; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hasting, Gregg
; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-115-286-1
Alignment Scores:
Pred. No.: 0 Length: 4014
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 16 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-115-286-1 (1-4014)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 466 ATGCAGCGAGCTGTGCCCGAGGGTTCCGAAGGCGCAAGCTGGGCGAGCGCATGGGGAAC 525

Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db 526 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGSCCCGTACCCACGGCTGTCTGTCTCGCC 585
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluAspGluGluLeu 60
Db 586 GCGGCGCTACTGGCGCTGTGGGACGCACTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA 645
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 646 GTGGTCCGGAGCTGGAGCGCGCCCGGGACACGGGACCAACGCGCTTCCGCTTGCAGGCC 705
Qy 81 PheAspGlnGlnLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 706 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGGCGCGGCTTC 765
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 766 ACGCTCCAGAACCTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAAACCGACCTG 825
Qy 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 826 GCGACTGTCTTCTCTCCGSCACCGTGATGGCGATCCAGCTCGGCTGCGGCTCAGC 885
Qy 141 LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheIleGlnPro 160
Db 886 CTCTGCGAGCGCTGCGCGCGCTTCTACTGCTGGGGGAGGCGTATTTTCATCCAGCG 945
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 946 CTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGAGAGCGCGCGCACCA 1005
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1006 CTACAGTTCCACTCTCTCGCGCGGATTCGACAGGGCGACGTAGGGCGCACGTCGGGGTC 1065
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1066 GTGACGACGAGCGCGCGCGCTGGGAAAGCGAGACCGAGAGCGAGGAGGACT 1125
Qy 221 GluGlyGluAspGluGlyProGlnThrSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1126 GAGGCGGAGGACGAAAGGGCTCAGTGGTCCCGCAGACCGCGCACGTGCAAGGCGTAGGA 1185
Qy 241 GlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHisArgTyVal 260
Db 1186 CAGCCACAGAACTGGAGCATAAAGAAAGCGGATTTGTTCAGTCCCGCTATGTG 1245
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1246 GAAACCATGCTTGTGGCAGACCACTGATGGCAGATTCACCGCAGTGGTCTAAAGCAT 1305
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrIysHisProSerIleArgAsn 300
Db 1306 TACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCGAGCATTCGTAAT 1365
Qy 301 SerValSerLeuValValValIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1366 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAGAGGGGCGGAA 1425
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1426 GTGACCTCCAATGTGCTCCCTCACTCTCGCGGAACCTTTTGGCAACTGGCAGAGCAGCACAA 1485
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGluAsp 360
Db 1486 CCACCCAGTACCGGGATGCAGAGCACTATGACACAGCAATTTCTTTCCACAGACAGGAC 1545
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1546 TTGTGTGGGTCCACAGCATGTGATGATACTCTTGGGATGGCTGATGTGGAACTGTGTGTGAT 1605

QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
DB 1606 CCGAGCAGAGAGCTGCTCCGTCATAGAGATGATGGTTTACAAGCTGCCCTTCCACAGCC 1665
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 1666 CATGAATTAGGCCACCGTGTAAACATGCCACATGATGCAAGACAGTGTGCCAGCCTT 1725
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1726 AATGGTGTGAACGAGATTTCCACATGATGGGGTCAATGCTTTTCCAACCTGGACACACAGC 1785
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1786 CAGCCTTGCTTCCCTGAGTCGCTACATGATTAATCATATTTCTGGATTAATGTCATGGG 1845
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1846 GAATGTTTGATGGACAAGCCTCAGAATCCATACAGCTCCAGGGGATCTCCCTGGCACC 1905
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1906 TCGTAGCATGCCAAGCGGAGTCCAGTGTATCATTTTGGGGAGGACTCCAAAACACTGCCCT 1965
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1966 GATGAGCCAGCACATGTAGACCTTGTGTGTATCCGGCACCTCTGGTGGGGTGTGTGGTG 2025
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 2026 TGTCAAAACAAACACTTCCCGTGGCGGATGCCAGCTGTGGAGAGGAAATGGTGT 2085
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 2086 ATCAACGGCAAGTGTGTAAACAAACCCGACAGAAAGCAATTTTGATACGCCCTTTTTCATGGA 2145
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
DB 2146 AGCTGGGNAATGTGGGGCTTGGGAGACTGTTTCAGAACCTGTGGTGGAGAGTCCAG 2205
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
DB 2206 TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC 2265
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 2266 AAACGAGTGCCTACAGATTCCTGTAACTTGTAGGACTGTCCAGACAAATATGGAAGAACCC 2325
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2326 TTTAGAGAGAACATGTGAGACACACACAGATTTTCAAAGCTTCCCTTGGAGTGGG 2385
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2386 CCTGGGTGGATGGATTCCAAGTACGCTGCGCTCTCAACAAAGACAGGTGCAAGCTC 2445
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2446 ATCTGCCAAGCAAGGCAATGGCTACTCTTCTGTTTTTCAGCCCCAAGGTTTGTAGATGT 2505
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyCysValLysAlaGly 700
DB 2506 ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGGT 2565
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2566 TGTGATCGCATCATAGACTCCAAAAGAAAGTTGATAAATGTGTTTTCGGGGGGAAAT 2625
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
DB 2626 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTAGGCAAAACCTGGATATCATGAT 2685
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760

DB 2686 ATCATCACAAATTCCAACTGGAGCCACCAACATCGAAGTGAACACGCGAACACAGGGGA 2745
QY 761 SerArgAsnAsnGlySerPheLeuAlaLysAlaLysAlaAspGlyThrTyrIleLeuAsn 780
DB 2746 TCCAGGAAACAATGGCAGCTTTCTTGCCATCAAGCTGTGTGATGGCACATATATCTTAAT 2805
QY 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
DB 2806 GGTGACTACATTTGTCCACCTTAGCAGCAAGACATATATGTACAAAGGTGTTGTCTTGAGG 2865
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
DB 2866 TACAGGGCTCTCTCGGCATTTGGAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2925
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
DB 2926 TTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATACACCTAC 2985
QY 841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
DB 2986 TTCGTAAGAAGAAGAAATCTTTCAATGCTATCCCCACCTTTTCAGCATGGGTCAIT 3045
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
DB 3046 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTTGGCAGAGAAGCTGGTAGAA 3105
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
DB 3106 TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 3165
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
DB 3166 ACCAGACCTTGTGACAGACCTCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3225
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
DB 3226 TCTAAGACCTGTGGGAAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATGTGGA 3285
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
DB 3286 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3345
QY 961 CysThrMetAlaGluCysSer 967
DB 3346 TGCACATGGCAGATGCACT 3366

RESULT 4

US-10-757-450-1
; Sequence 1, Application US/10757450
; Publication No. US20040175794A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/757,450

FILING DATE: 15-Jan-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/115,286
 FILING DATE: 04-Apr-2002
 APPLICATION NUMBER: 08/845,496
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-70000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4014 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-757-450-1

Alignment Scores:
 Pred. No.: 0 Length: 4014
 Score: 5232.00 Matches: 957
 Percent Similarity: 99.38% Conservations: 4
 Best Local Similarity: 98.97% Mismatches: 6
 Query Match: 98.96% Indels: 0
 DB: 18 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-757-450-1 (1-4014)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
 DB 466 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGCGCGAAGCTGGCGAGCGAGCATGGGGAAC 525
 QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
 DB 526 GCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGGCCGTATCCACGCTGCTGCTGCC 585
 QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
 DB 586 GCGCGCTACTGGCCGTGTGGACGCACTCGGGCCGCCCTCCGAGGAGGAGCGAGGCTA 645
 QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
 DB 646 GTGGTCCGAGCTGGAGCGGCCCGCGGACACGGGACACGCGCTCCGCTGCACGCC 705
 QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
 DB 706 TTTGACGAGCTGGATCTGGAGCTCGGCCCGCCACAGCAGCTTTTGGGGCCCGGCTTC 765
 QY 101 ThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGluThrAspLeu 120
 DB 766 ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAAACCGCAGCTG 825
 QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
 DB 826 GCGCACTGCTTACTTCGGCACCGCTGATGGCGATCCACGCTCGGCTCGGCCCTCAGC 885
 QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro 160
 DB 886 CTCTGCGAGCGGTGCGCGGCCCTTACTCTGGGGAGGGGTATTTTCATCCAGCG 945
 QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
 DB 946 CTGCCCCCGCCAGCGAGCGCTCGCCACCGCCCGCCAGGGGAGAGCGCGCGCACCA 1005
 QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200

DB 1006 CTACAGTTCACCTCTCTCGCGCGGAATCGCGAGGGCGACGTAGCGGCACGTGCGGGTC 1065
 QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
 DB 1066 GTGGACGACGAGCCCGCGCGCTGGGAAAGCGAGACCGAAGGAGGACT 1125
 QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
 DB 1126 GAGGGCGAGGACGAAGGGCTCAGTGGTCCGCCAGGACCCCGCACTGCAAGGCGTAGGA 1185
 QY 241 GlnProThrGlyThrGlySerLeuArgLysValSerPheValSerSerHisArgTyrVal 260
 DB 1186 CAGCCACAGGAAGCTCGAAGCATAGAGAGACGATTTGTGTCCAGTCAACCGCTATGTG 1245
 QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
 DB 1246 GAAACCATGTTGTGGCAGACCATGTCGATGGCAGAAATTCACGCGAGTGGTCTAAAGCAT 1305
 QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerLeuArgAsn 300
 DB 1306 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCACGATTCGTAAT 1365
 QY 301 SerValSerLeuValValValLysLeuValLysLeuValLysLeuValLysLeuValLys 320
 DB 1366 TCAGTTAGCTGTGGTGGTGAAGATCTTGTGTATCCACGATGAACAGAGGGGCCGAA 1425
 QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
 DB 1426 GTGACCTCCATGCTGCCCTCACTCTGGCGAATTTTGGCAATGGCAGAGCAGCAAC 1485
 QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaLeuLeuPheThrArgGlnAsp 360
 DB 1486 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTTCTTTCCACGAGCAGGAC 1545
 QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
 DB 1546 TTGTGTGGGTCCAGACATGTGATCTTTGGGATGGCTGATTTGGAACTGTGTGTAT 1605
 QY 381 ProSerArgSerCysSerValLysGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
 DB 1606 CCAGCGAGAGCTGCTCCGTCATAGAGATGATGGTTTACAGCTGCTTCCACACAGCC 1665
 QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
 DB 1666 CATGAATTAGGCCACGCTGTTTAAACATGTCACATGATGATGCAAGCAGTGTGCGAGCTT 1725
 QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
 DB 1726 AATGGTGTGAACGAGGATTCACATGATGGCGTCAATGCTTTTCAACCTGGACACAGC 1785
 QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
 DB 1786 CAGCTTGGTCTCTTGGAGTGGCTACATGATTTACATCATTTCTGGATATGTCATGGG 1845
 QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
 DB 1846 GAATGTTGATGACAAAGCTCCAGATCCCATACAGCTCCAGCGCATCTCCCTGGCACC 1905
 QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
 DB 1906 TCGTACGATCCAAACCGCGAGTGCAGTTTACATTTTGGGGAGGACTCCAAACACTGGCCT 1965
 QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
 DB 1966 GATGACGACGACATAGTACACCTTGTGTGTATCCGCGACCTCTGTGTGGGTCTGGTG 2025
 QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
 DB 2026 TGTCAACCAACACACTTCCCGTGGCGGATGGCACAGCTGTGGAGAAGGAAATGGTGT 2085
 QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
 DB 2086 ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGTATACGCTTTTTCATGGA 2145

QY 561 SerTyrGlyMetTyrProTyrGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 2146 AGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCGAGAACGTGCGGTGGAGAGTCCAG 2205
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 2206 TACACGATGAGGGAATGTGACAACTCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGC 2265
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2266 AAACGAGTGGCTACAGATCTCTGTACCTTGAAGTGTGAGGACTGTCCAGACAAATATGAAAAACC 2325
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2326 TTTAGAGAGAACATGTGAGACACACAGAGTTTCAAAAGCTTCTTTGGAGTGGG 2385
QY 641 ProAlaValGluTyrPheProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2386 CTGCGGTGGATGGATCCCAAGTACGCTGGGCTCTACCAAGAGCAGAGTGCAGCTC 2445
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2446 ATCTGCCAAGCCAAAGGCAATGGCTACTTCTGTTTTCAGCCCAAGGTTGTAGTGT 2505
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyClnCysValLysAlaGly 700
Db 2506 ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAGCTGTG 2565
QY 701 CysAspArgIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2566 TGTGATCGCATCATAGACTCCAAAAAGAGTTGTATAATGTGTGTGCGGGGAAAT 2625
QY 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2626 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2685
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2686 ATCATCACAAATCCAACTGAGGCCAACCAATCGAAGTGAACAGCGGAAACAGAGGGA 2745
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2746 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAAGCTGCTGATGGCACATATATCTTAAT 2805
QY 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2806 GGTGACTACACTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGGTGTCTGTGAGG 2865
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2866 TACAGCGGCTCTCTGCGGCATTTGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGCCC 2925
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2926 TTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATACACCTAC 2985
QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2986 TTTCGTAAGAAGAAGAAGAAATCTTTCAATGTCTATCCCACTTTTTCAGCATGGGTCAAT 3045
QY 861 GluGluTyrGlyCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGlu 880
Db 3046 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTGGCAGAAAGACTGTGTAGAA 3105
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TGCCGAGACATTAATGCACAGCTGCTTCCGAGTGTGCAAGAAAGTGAAGCCAGCCAGC 3165
QY 901 ThrArgProCysAlaAspHisProCysProGlnTyrGlnLeuGlyClnTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGCAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCAATCATG 3225

QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3226 TCTAGACCTGTGGAGAGGTTACAAAAAGAAAGCTTGAAGTGTCTGCTCCCATATGGA 3285
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3345
QY 961 CysThrMetAlaGluCysSer 967
Db 3346 TGCACATGGCAGATGCAGT 3366
RESULT 5
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-10-105-929-1
Alignment Scores:
Pred. No.: 0 Length: 4676
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 13 Gaps: 0
US-09-373-658c-126 (1-967) x US-10-105-929-1 (1-4676)
QY 1 MetGlnArgAlaValProGluGlyPheGlyArgAlaGlyLeuGlySerAspMetGlyAsn 20
Db 460 ATGCAGCAGCTGTGCCGAGGGGTTCGGAAGCGCAAGCTGGCGACGACATGGGGAAC 519
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 520 GCGAGCGGGCTCCGGGCTCTCGAGCTTGGGCGGTACCCAGCGCTGCTGCTCGCC 579
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 580 GCGGCGCTACTGCGCGTGTGCGACCACTCGGGCGCCCTCCGAGGAGACGAGGAGCTA 639
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 640 GTGGTGCCGAGCTGGAGCCGCCCGGACACCGGACCCAGCGCTCTCGCTGACAGCC 699
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 700 TTTGACACGACCTGGATCTGGAGCTGCGGCCCGCAGCAGCTTTTGGCGCCGCGCTTC 759
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 760 ACGCTCCAGAACGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGAACCCGACCTG 819

121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
820 GGCACGTCTTACTCCGGCACCGTGANTGGGATCCACAGCTCGGCTCGCCCTCAGC 879
141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro 160
880 CTCGCGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGCGGTATTTTCATCCAGCGC 939
161 LeuProAlaAlaSerGluAlaGluLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
940 CTGCGCGCGCGCAGCGCGCTTCGCCACCGCCCGCCGAGGAGGAGCGCGCGCACCA 999
181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
1000 CTACAGTTCACCTCTCTGCGCGCGGATCGCGAGGGCGAGCTAGCGCGCAGCTGCGGGGTC 1059
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluGlyThr 220
1060 GTGGACGACGAGCCCGCGCGCATGGGAAAGCGGAGACCGGAGACGAGGAGGACT 1119
221 GluGlyGluAspGluGlyProGlnTTPSerProGlnAspProAlaLeuGlnGlyValGly 240
1120 GAGGGCGAGGACGAAGGGCTCAGTGGTCCGCCAGGACCCCGGCATCTGCAAGGCGTAGGA 1179
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
1180 CAGCCACACAGGAATCTGGAGCATAGAGAGAGCGATTTGTGTCCAGTCAACCGCTATGTG 1239
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
1240 GAAACCATGCTGTGGCAGACACCATGCGAGAGATTCACCGCAGTGGTCTAAAGCAT 1299
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
1300 TACCTTCTCAGCTGTGTTTTCGGTGGCAGCCAGATGTGACAAACACCCCGCAGCATTCGTAA 1359
301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
1360 TCAGTTAGCTGTGTGTGTGTGAAGATCTTGTTCATCCAGTGAACAGAGGGGCGCGAA 1419
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
1420 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGGCAACTGGCAGAGCAGCAAC 1479
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
1480 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATCTTTTCCACGACAGGAC 1539
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
1540 TTGTGTGGGTCACAGACATGTGATCTCTTGGGATGCTGATGTGGACTGTGTGTGAT 1599
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
1600 CCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1659
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
1660 CATGAATTAGCGCCACGTGTTTAAACATGCCATGATGATGCAAGCAGTGTGCGAGCCTT 1719
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1720 AATGGTGTGAACACAGGATCCCATGATGCGGTCAATGCTTCCAACTCTGGACACAGC 1779
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1780 CAGCCTTGGTCTCTTGCAGTGCCTACATGATTTACATCATTTCTGGATATGTGTATGGG 1839
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1840 GAATGTTTGTGACAGACCTCAGAAATCCCATACAGCTCCGAGCGCATCTCCCTGGCAC 1899

481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1900 TCGTACGATGCCAACCGCGCAGTCCAGTTTACATTTGGGGAGGACTCCAAACACTCCCC 1959
501 AspAlaAlaSerThrCysSerThrLeuTTPCysThrGlyThrSerGlyGlyValLeuVal 520
1960 GATGCAGCCAGCACATGTAGCACCTTGTGTGTATCCGGCACCTCTGTTGGGTGCTGGTG 2019
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
2020 TGTCAAAACCAACACTTCCGTTGGGCGATGGCACCAGCTGTGCGAAGAGGAAATGGTGT 2079
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
2080 ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGTATACGCTTTTTCATGGA 2139
561 SerTTPGlyMetTTPGlyProTTPGlyAspCysSerArgThrCysGlyGlyValGln 580
2140 AGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCGAGAACCTGCGTGGAGGAGTCCAG 2199
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
2200 TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC 2259
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
2260 AAACGAGTGGCTTACAGATCTCTGTAACTTGGAGACTGTCCAGACAAATATATGAAAAC 2319
621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
2320 TTTAGAGAGGAACAAATGTGAAGCACCAACGAGTTTTTCAAAAGCTTCTTTGGAGTGGG 2379
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2380 CCTGCGGTGGATGGATTTCCAGTACGCTGGCGTCTCCACCAAGSACAGCTGCAAGCTC 2439
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2440 ATCTGCAAGCAAGGCAATGGCTACTTCTCTGTTTTCAGACCCCAAGGTGTAGATGGT 2499
681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
2500 ACTCCATGTAGCCCAATTCACCTCTGTCTGTGTCAGAGACAGTGTGTAAAGCTGGT 2559
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2560 TGTGATCGCATCATAGACTCCAAAGAGAGTGTGATAAATGTGTGTTCGCGGGGAAAT 2619
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2620 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCATAAACCTGGATATCATGAT 2679
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
2680 ATCATCAAAATCCAACTGGAGCCCAACATCGAAGTGAACAGCGGAAACAGAGGGA 2739
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
2740 TCCAGGAACAAATGGCAGCTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAT 2799
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2800 GGTGACTTACACTTTGTCCACTTTAGAGCAAGACATATGATACAAAGGTGTGTCTTGAGG 2859
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLysLeuGluPro 820
2860 TACAGCGGCTCTCTGCGCATTTGGAAGAAATTTGCGAGCTTTAGCCCTCTCTCAAGAGGCC 2919
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
2920 TTGACCATTCAGGTTCTTACTGTGGGCATGCCCCCTTCGACTAAATTAATACACCTAC 2979
841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860

421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1268 AATGGTGTGAACCGATTCACATGATGGCTCAATGCTTCCAACTGGACCAAGC 1327
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1328 CAGCCTTGGTCTCTTGGAGTGCCTACATGATGATACATCATTTCTGGATAATGGTCATGGG 1387
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1388 GAATGTTTGTATGACAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTCCCTGGCACCC 1447
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1448 TCGTAGCATGCCAACCGCGAGTCCAGTTTACATTTTGGGGAGGACTCCAAACACTGCCCT 1507
501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
1508 GATGAGCCAGCAGCATGTAGCACCCTTGTGTGTACCGGCACCTCTGTGGGGTGTGGTG 1567
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
1568 TGTCAAAACCAACACTTCCCGTGGCGGATGGCACCAGCTGTGGAGAGGAGAAATGGTGT 1627
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCATTTTGTATGCCCTTTTTCATGGA 1687
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
1688 AGCTGGGGAATGTGGGGCCCTTGGGAGACTGTTCGAGACGTGGCGTGGAGGATCCAG 1747
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
1748 TACACGATGAGGAATGTGCAACCCAGTCCCAAGAAATGGAGGAGTACTGTGGAAGGC 1807
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
1808 AAACGAGTGGCTACAGATCTGTAACTTGTAGACTGTCCAGACATATATGAAANAACC 1867
621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
1868 TTTAGAGAGGACATGTGAGCACACACAGAGTTTCAAAGCTTCTTTTGGAGTGGG 1927
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysProLysLysLeu 660
1928 CCTGGGTGGAATGGAATCCCAAGTACGCTGGCTCTCACCAGAGGACAGGTGCAAGCTC 1987
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
1988 ATCTGCCAGCCAAAGCAATGGCTACTTCTTCTGTGTGCAAGCCCAAGTTGTAGATGGT 2047
681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
2048 ACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTGGT 2107
701 CysAspArgIleLeuAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2108 TGTGATCCCATCATAGACTCCAAAGAAAGTTTGTATAATGTGTGTGTGGGGGGAAT 2167
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2168 GGATCTACTTGTAAAAAATATACAGATCAGTACTAGTGTGCAAAACCTGGATATCATGAT 2227
741 IleIleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
2228 ATCATCAATTCATCTGGAGCCACCAACATCCAGTGAACACAGCGGACCAAGAGGGA 2287
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
2288 TCCAGGAACAATGGCAGCTTCTTGTGCCATCAAGCTGTGTGTCACATATATCTTAAAT 2347

781 GlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2348 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAAGGTGTGTCTTGAGG 2407
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
2408 TACAGCGGTCTCTCGCGCATTTGGAAAGAATTCGACGCTTTAGCCCTCTCAAAGAGCCC 2467
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
2468 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2527
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
2528 TTCGTAAGAAGAAGAAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2587
861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
2588 GAAGAGTGGGGCGAATGTTCTTAAGTCATGTGAATGGGTTGGCAGAGAAGACTGGTAGAA 2647
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
2648 TGCCGAGACATTAATGACAGCCTGTCTCGAGTGTGCAAGAGAGTGAAGCCAGCCAGC 2707
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
2708 ACCAGACCTTGTGCAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 2767
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
2768 TCTAAGACCTGTGGGAAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGA 2827
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
2828 GGGGTGTATCTCATGAGACTGTGATCCTTTAAGAAACCTTAACACATTTTCATAGACTTT 2887
961 CysThrMetAlaGluCysSer 967
2888 TGCACAATGGCAGATGCACT 2908

RESULT 7
US-10-210-120-57
; Sequence 57, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Ruben, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 4309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-57

Alignment Scores:
Pred. No.: 0 Length: 4309
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 16 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-210-120-57 (1-4309)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
DB 116 ATGCAGCAGCTGTGCCCCAGGGGTTTCGAAAGCGCAAGCTGGCGACGACATGGGGAAC 175
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 176 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGCCAGTACCCACGCTGCTGCTCGCC 235
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
DB 236 CGGGCGCTACTGGCCGTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGCAGGAGCTA 295
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
DB 296 GTGGTCCGGAGCTGAGCGCGCCCCGGGACACGGGACACCGCGCTCCGCTCGCACGCC 355
QY 81 PheAspGlnGlnLeuAspLeuValProProAspSerSerPheLeuAlaProGlyPhe 100
DB 356 TTTGACCAGACGTGGATCTGGAGCTCGCGCCGCGACAGCAGCTTTTGGGGCCCGGCTTC 415
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 416 ACGCTCCAGACGTGGGGCGCAATCCGGGTCCGAGACCGCTTCGGGAAACCGACCTG 475
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
DB 476 GGGCACTGCTTCTACTCCGGCACCGGAATGCGATCCCACTCGGCTCGCCCTCCAGC 535
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 536 CTCGCGAGGGCGTGGCGCGCTTCTACCTGCTGGGGAGGCGTATTTTCATCCAGCCG 595
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
DB 596 CTGCGCGCGCCAGCAGCGCTCGCCACCGCGCCGCCAGGGGAGAAAGCGCGGCCCA 655
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
DB 656 CTACAGTTCACCTCTCGCGCGGAATCGCGAGGGCGAGCTCGCGGCGACGTCGCGGGTC 715
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 716 GTGGACGACGACCCCGCGGACTGGGAAGCGGAGACCGAAGACGAGCGAGGACT 775
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 776 GAGGGCGAGGAGGAGGCTCAGTGGTCCCGCGCAGGACCCGCGCACTGCAAGGCGTAGGA 835
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 836 CAGCCCAAGGAACCTGGAAGCATAGAAAGACGGATTTGTCTCCAGTCACCGCTATGTG 895
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 896 GAAACCATCTGTGGCAGACCACTGATGGCAGAAATCCACGGCAGTGTCTAAAGCAT 955
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 956 TACCTTCTCACGTGTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCCGCAGCATTCGTAA 1015
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 1016 TCAGTTAGCTGTGGTGGTGAAGATCTTGGTCAATCCAGCATGAACAGAAAGGGCCGGAA 1075
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 1076 GTGACCTCAATGCTGCCCTCACTCTGCGGAACCTTTTGCACCTGGCAGAAAGCAGCAAC 1135
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
DB 1136 CCACCGAGTGACGGGATGACAGCACTATGACACAGCAATTCCTTTTCCACGACAGGAC 1195

QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
DB 1196 TTGTGTGGGTCCACACATGTGATACTCTTGGATGGCTGATGTTGGAACTGTGTGTGAT 1255
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
DB 1256 CCGAGCAGAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTGCCTTCCACACAGCC 1315
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 1316 CATGAATTAGCCACGCTGTTTAACATGCCACATGATGATGCAAAAGCAGTGTGTCAGCCTT 1375
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1376 AATGGTGTGAACAGAAATCCACATGATGGCGTCAATCTTTCCAACTGGACACAGC 1435
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1436 CAGCCTTGGTCTCTCTCGAGTGCCTACATGATTAACATCATTTCTGGATAATGGTCATGG 1495
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1496 GAATGTTTGAATGGCAAGCCTCAGAAATCCATACAGCTCCCAAGCGATCTCCCTGGCACC 1555
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1556 TCGTAGATGCCACCGGAGTGCACGTTTACATTTGGGGAGGACTCCAAACACTGCCCCC 1615
QY 501 AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1616 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGTTGGGTGCTGGTG 1675
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 1676 TGTCAAAACAAACACTCTCCGTGGCGGATGCCACAGCTGTGGAGAAAGGAAATGGTGT 1735
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 1736 ATCAACGGCAGTGTGTGNACAAACCCGACAGAAAGCATTTTGATACGCTTTTCATGGA 1795
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
DB 1796 AGCTGGGAATGTGGGGCTTGGGGAGACTGTTCCAGAACTGCGGTGGAGAGTCCAG 1855
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
DB 1856 TACACGATGAGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGC 1915
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 1916 AAACGAGTGGCTACAGATCCTGTAACTTGAGGACTGTCCAGACATATAATGGAAAAACC 1975
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 1976 TTTAGAGAGGAACAATGTGAACACACACAGAGTTTCAAAAGCTTCTTTTGGAGTGGG 2035
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2036 CTGCGGTGGGAATGATTTCCCAAGTACGCTGGCGTCTCAACAAAGACAGGTGCAAGCTC 2095
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2096 ATCTGCCAAGCCAAAGGCATTTGGTACTTCTTCTGTTTTCAGCCCCCAAGGTGTAGATGT 2155
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
DB 2156 ACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGAGGACAGTGTGTAAAGTGTGT 2215
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2216 TGTGATCGCATAGACTCCAAAGAAAGTTTGATAAATGTGTGTGTTTCCGGGGGAAT 2275
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db 2276 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAGAAACCTGGATATCATGAT 2335
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValysGlnArgAsnGlnArgGly 760
Db 2336 ATCATCACAATTCACATGGAGCCACCAACATCGAAGTGAACAGCGGACCAAGAGGGGA 2395
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleValAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2396 TCAGAGAACATGGCAGCTTCTTGCCATCAAGCTGCTGATGGCACAATATCTCTAAT 2455
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrIysGlyValValLeuArg 800
Db 2456 GGTGACTACATTTGTCCACTTAGAGCAAGACATTATGTACAAAGGTGTGTCTTGAGG 2515
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuIysGluPro 820
Db 2516 TACAGCGGCTCTCTGGCGCATTTGGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2575
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProIysIleIysTyrThrTyr 840
Db 2576 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATATACCTAC 2635
Qy 841 PheValIysIysIysGlySerPheAsnAlaIleProThrPheSerAlaIleValIle 860
Db 2636 TTCGTAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 2695
Qy 861 GluGluTrpGlyGluCysSerIysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2696 GAAGAGTGGGGCGAATGTTCTAAGTCTATGTGAATTTGGTGGCAGAGAAGACTGGTAGAA 2755
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaIysGluValIysProAlaSer 900
Db 2756 TCCGAGACATTAATGACAGACCTGCTTCGAGTGTGCAAGGAAGTGAAGCAGCCAGCAGC 2815
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2816 ACCAGACTTGTGCAGACCATCCCTGCTCCCGCAGTGGCGAGTGGTTCATCATGT 2875
Qy 921 SerIysThrCysGlyIysGlyTyrIysIysThrSerLeuIysCysLeuSerHisAspGly 940
Db 2876 TCTAAGACCTGTGGAGGGGTACAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGA 2935
Qy 941 GlyValIleSerHisAspSerCysAspProLeuIysIysProIysHisPheIleAspPhe 960
Db 2936 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCATAGACTTT 2995
Qy 961 CysThrMetAlaGluCysSer 967
Db 2996 TGCACAAATGGCAGATGCAGT 3016

RESULT 8

US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Alignment Scores:
Pred. No.: 0 Length: 4447
Score: 5224.00 Matches: 955
Percent Similarity: 99.28% Conservatives: 5
Best Local Similarity: 98.76% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 18 Gaps: 0
US-09-373-658c-126 (1-967) x US-10-755-889-133 (1-4447)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgIysLeuGlySerAspMetGlyAsn 20
Db 243 ATGCAGCAGCTGTGCGCGAGGGGTTTCGGAAGGCGCAAGCTGGCGACGACATGGGGAAC 302
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 303 GCGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCGGCTATCCCACTGTGTCTGTCTGCC 362
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 363 GCGGCGCTACTGGCGCTGTGCGACGCACTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA 422
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 423 GTGGTCCGAGCTGGAGCGCGCCCGGGACACCGGACACACGCGCCTCCGCTCGCACGCC 482
Qy 81 PheAspGlnLeuLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACGACGAGCTGGAATCTGGAGCTGGCGCCCGACAGCAGCTTTTGGCGCCCGGCTTC 542
Qy 101 ThrLeuGlnAsnValGlyArgIysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACCTCCAGAACCTGGGGCGCAATTCGGGTCCGAGACGCGCTCCGGAAACCGACCTG 602
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 603 GCGCACTGTCTTACTCCGCGACCGTGAATGGCGATCCCACTCGGCTCGCGCTCGCTCAGC 662
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 663 CTCTGGAGGGCGTGGCGGCGCTTCTACCTGCTGGGGAGGCGGTATTTTCATCCAGCCG 722
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysProProAlaPro 180
Db 723 CTGCGCGCGCCAGCGAGCGCTTCGCCACGCGCGCCCGCAGGGGAGAGCCCGCGCACCA 782
Qy 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 783 CTACAGTTCCACTCTCTGCGCGGAATCGGAGGCGACCTAGCGCGGCGACGTGCGGGGTC 842
Qy 201 ValAspAspGluProArgProThrGlyIysAlaGluThrGluAspGluGlyThr 220
Db 843 GTGCAGCAGCGAGCCCGCGCGCATGGGAAGCGGAGACCCGAAGACGAGGAGGAGACT 902
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 903 GAGGGCGAGGACCGAGGGCTCAGTGGTCCCGCAGGACCCCGGCACTGCAAGGCGTAGGA 962
Qy 241 GlnProThrGlyThrGlySerIleArgIysLeuArgPheValSerSerHisArgTyrVal 260
Db 963 CAGCCCAACAGAACTGGAGCATTAAGAAAGACGATTTGTCTCAGTCCAGTCCCGCTATGT 1022
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuIysHis 280
Db 1023 GAAACCATGTTGTGGCAGACCACTGATGCGAGATTCACGCGCATGTGTCTAAGCAT 1082
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrIysHisProSerIleArgAsn 300
Db 1083 TACCTTCTCAGTGTGTTCGTGGCAGCCAGATTTGTACAAACACCCAGCATTCGTAT 1142
Qy 301 SerValSerLeuValValIysIleLeuValIleHisAspGluGlnIysGlyProGlu 320

Db 1143 TCAGTTAGCCTGGTGGTGAAGATCTTTGGTCAATCCACGATGAACAGAGGGCGCGAA 1202
Qy 321 ValThrSerAsnAlaLeuThrLeuArgAsnPheCysAsnTrpGlnYsGlnHisLeu 340
Db 1203 GTGACCTCCAAATGCTGGCCCTCACTCTGGGGAATTTTGAACCTGGCAGAGCAGCAAC 1262
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1263 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCCTTTCCACAGACAGAC 1322
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1323 TTGTGTGGGTCCACACATGTGATCTCTTGGGATGGCTGATGTGGAACTGTGTGTGAT 1382
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
Db 1383 CCGAGCAGAAGCTGCTCCGTATAGAAGATGAAGTTTACAAGCTGGCTTCACCAAGCC 1442
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLeuGlnCysAlaSerLeu 420
Db 1443 CATGAATTAGGCCACGCTGTTAAACATGCCACATGATGATGCAAGAGCTGTGCCAGCCTT 1502
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1503 AATGGTGTGAACACGAGATTCACCATGATGGCGTCAATGCTTTTCCAACCTGGACACACAGC 1562
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1563 CAGCCTTGGTCTCCCTTGACAGTCCCTACATGATATACATCAATTTCTGGATAATGGTCATGGG 1622
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1623 GAATGTTTGTATGGACAGCTCAATATCCATACAGCTCCAGGGCACTCCCTGGCACC 1682
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1683 TCGTACGATGCCAAACCGGCAGTGCAGTTTACATTTGGGGAGGACTCCAAAACACTGCCCT 1742
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1743 GATGACGCAGCAGCATGATGACACCTTGTGGTGTACCGGCACCTCTGGTGGGGTGTGGTG 1802
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGlyGlyLysTrpCys 540
Db 1803 TGTCAAAACCAACACTTCCCGTGGCGGATGCCACAGCTGTGGAGAGGAAATGGTGT 1862
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1863 ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCAATTTGTATACGCTTTTCATGGA 1922
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 1923 AACTGGGGAATGTGGGGCTTTGGGAGACTGTTCGAGAACGTGGCGTGGAGAGTCCAG 1982
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 1983 TACACGATGAGGGATGTGACAAACCCAGCTCCCAAGAGATGGAGGAGTACTGTGAAGC 2042
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2043 AAACGAGTGCCTACAGATCTGTAACTTGAACCTTGAGGACTGTCCAGACAAATAATGGAAAAACC 2102
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2103 TTTAGAGAGGAACAATGTGAAGCACACACGAGTTTTTCAAGAGCTTTTCAAGAGTGGG 2162
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2163 CTGCGGTGGATGGATTTCCCAAGTAGCTGGCGTCTCAACCAAGACAGAGTGAAGCTC 2222
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2223 ATCTGCCAAGCCAAAGGCATTTGGTACTTCTTCGTTTTTGCAGCCCAAGGTTTGTAGTGT 2282

Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db 2283 ACTCATGTAGCCAGATTCACCTCTGTCTGTGTGTCAGGACAGTGTGTAAAACTGGT 2342
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2343 TGTGATCGCATCATAGACTCCAAAAAGAGTTTGATAAATGTGGTGTTCGGGGGAAAT 2402
Qy 721 GlySerThrCysLysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisLeu 740
Db 2403 GGATCTACTTGTAAAAAATATACAGATCAGTTACTAGTGCAAAAACCTGGATATCATGAT 2462
Qy 741 IleIleThrIleProThrGlyValAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2463 ATCATCACAATTCNACTGGAGCCACCAACATCGAAGTGAACAGCGGACACAGAGGGA 2522
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2523 TCCAGGAACAATGGCAGCTTTCTTGCATCAAGCTGCTGATGGCACATATATCTTAAT 2582
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2583 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATATTGTACAAAGGTGTTCCTTGAGG 2642
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2643 TACAGCGCTCTCTCGCGCATTTGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCC 2702
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2703 TTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAAATACACCTAC 2762
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2763 TTCGTAAAGAGAAGAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2822
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2823 GAAGATGGGGCGAATGTTCTAAGTCATGTGAATGGTGGCAGAGAAGACTGGTAGAA 2882
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2883 TGCCGAGACATTAATGAGCAGCTCTCTCCGAGTGTGCAAGGAAAGTGAAGCAGCCAGC 2942
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2943 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3002
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3003 TCTAAGACTGTGGAGAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGCCCATGTGGA 3062
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3063 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3122
Qy 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCAAAATGGCAGAATGCAGT 3143

RESULT 9

US-10-159-563-192

; Sequence 192, Application US/10159563

; Publication NO. US20040009154A1

; GENERAL INFORMATION:

; APPLICANT: Khan, Javed

; APPLICANT: Ringner, Markus

; APPLICANT: Peterson, Carsten

; APPLICANT: Meltzer, Paul

; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

; FILE REFERENCE: 11613.56US11

1 CURRENT APPLICATION NUMBER: US/10/159,563
2 CURRENT FILING DATE: 2002-12-09
3 PRIOR APPLICATION NUMBER: US 10/133,937
4 PRIOR FILING DATE: 2002-04-25
5 NUMBER OF SEQ ID NOS: 444
6 SOFTWARE: Patent in version 3.1
7 SEQ ID NO 192
8 LENGTH: 4459
9 TYPE: DNA
10 ORGANISM: Homo sapiens
11 US-10-159-563-192

Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5294.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 17 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-192 (1-4459)

QY	1	MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn	20
DB	243	ATGCAGCGAGCTGTGCCGAGGGGTTTCGGAAGCGCAAGCTGGGCGACGACATGGGGAC	302
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
DB	303	CGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCGCGTACCCACGCTGCTGCTCGCC	362
QY	41	AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu	60
DB	363	CGGGCGCTACTGGCGGTCTCGGACGCACTCGGGCGCCCTCCGAGGAGGACGAGGACTA	422
QY	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla	80
DB	423	GTGGTCCGAGCTGGAGCGCGCCCGGGACACGGGACACGCGCCCTCCGCTGCACGCC	482
QY	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
DB	483	TTTGACGAGCGCTGGAGCTCGGGCTCGGCGCCGACAGAGCTTTTGGCGCCCGGCTTC	542
QY	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu	120
DB	543	ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACCGCGCTCCGGAAACCGACCTG	602
QY	121	AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
DB	603	CGGCACCTGCTTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCAGC	662
QY	141	LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro	160
DB	663	CTTGGCAGGCGGTGCGCGCGCTTCTACTCTGGGGAGGCGTATTTTCATCCAGCCG	722
QY	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro	180
DB	723	CTGCCCGCGCCAGCAGAGCGCTCGCCACCGCGCCCGCCGAGGAGGAGCGCCGCCACCA	782
QY	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal	200
DB	783	CTACAGTTCACCTCTCTGCGCGGAAATCGGCGAGGCGACGTCGCGCGCACGTGCGGGTC	842
QY	201	ValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluGlyThr	220
DB	843	GTGGACACGAGCGCCCGCGACTGGGAAACCGGAGACCGAAGACGAGGAGGAGCT	902
QY	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
DB	903	GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	962
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
DB	963	CAGCCCAACAGAACTGGAAGCATAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1022

QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
DB	1023	GAACCATCTTGTGGCAGACCATCGATGGCAGAAATTCACGGCAGTGTCTTAAAGCAT	1082
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
DB	1083	TACCTTCTCACGTTGTTTTCGGTGGCAGCAGATGTACAAACACCCAGCATTCGTAAT	1142
QY	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
DB	1143	TCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAGGGGCGGAA	1202
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
DB	1203	GTGACCTCAATGCTGCTCCTCACTCTGCGAACTTTTGCAACTGGCAGAGCAGCAAC	1262
QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
DB	1263	CCACCAGTGACCGGGATGACAGAGCACTATGACACAGCAATCTTTTCCACAGAGGAC	1322
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	1323	TTGTGGGTCCACAGACATGTGATCTCTTGGATGGCTGATGTGGAACTGTGTGAT	1382
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla	400
DB	1383	CCGAGCAGAAAGCTGCTCCGTCTAGAAAGATGATGGTTTACAGCTGCTTCCACACAGCC	1442
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
DB	1443	CATGAATAGGCCACCGTGTAAACATGCCACATGATGATGATGATGATGATGATGATGAT	1502
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	1503	AATGGTGTGAACCAAGATTTCCACATGATGGCGTCAATGCTTTCCAACTTGGACACAGC	1562
QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	1563	CAGCTTGGTCTCTTCTGATGCTGCTATGATGATGATGATGATGATGATGATGATGATG	1622
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	1623	GAATGTTGATGACAGCGCTCCAGATCCCATACAGCTCCAGCGCGATCTCCCTGGCACC	1682
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	1683	TCGTACGATGCCAACCGCGAGTCCAGTTTACATTTGGGAGGAGCTCCAAACACTGCCCC	1742
QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	1743	GATGACGACGACATGATGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1802
QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	1803	TGTCAAAACCAACACTTCCGTTGGCGGATGGCAGCAGCTGTGGAGAGGAGGAGGAGGAG	1862
QY	541	IleAsnGlyLysCysValLeuLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	1863	ATCAACGCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATGACCTTTTTCATGA	1922
QY	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	1923	AGCTGGGAGATGTGGGGCTTGGGAGAGCTGTTCGAGAACGTCGCGTGGAGGAGTCCAG	1982
QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGlyGly	600
DB	1983	TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGGAGGAGGAGGAGG	2042
QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
DB	2043	AAACGAGTGGCTACAGATCTGTAACTTGTAGGAGCTGTCCAGACAATATATGAAAAACC	2102

621 PheArgGluGluGlnCysGluAlaHisAenGluPheSerLysAlaSerPheGlySerGly 640
Db TTTAGAGGAGCAATGTGACACACACACAGTCTTCAAAGCTTCTTTGGAGTGG 2162
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db CTGCGGTGGAATGGATCCCAAGTACGTGGCTCTCAACAAAGACAGGTGCAAGCTC 2222
661 IleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysValValAspGly 680
Db ATCTGCAAGCAAGGCAATGGCTACTTCTTCGTTTTCAGCCCAAGGTTTGTAGTGT 2282
681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db ACTCCATGTAGCCAGATTCACCTCTGTGTGTGCAAGGACAGTGTGTAAGCTGT 2342
701 CysAspArgIleAlaAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAen 720
Db TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAATGTGGTGTTCGCGGGGAAT 2402
721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisasp 740
Db GGATCTACTTGTAAAAAATATCAGATCAGTTACTAGTGCAAAACCTTGATCATGAT 2462
741 IleIleThrIleProThrGlyAlaThrAenIleGluValLysGlnArgAenGlnArgGly 760
Db ATCATCACAAATTCACCTGAGCCACCAATCGAAGTGAACAGCGGAAACAGAGGGA 2522
761 SerArgAsnAsnGlySerPheLeuAlaLysLysAlaAlaAspGlyThrTyrIleLeuAen 780
Db TCCAGGAACAATGGCAGCTTCTTCCATCAAAAGCTGTGTGTCACACATATATCTTAAT 2582
781 GlyAspTyrThrLeuSerThrLeuGlnGlnAspIleMetTyrLysGlyValValLeuArg 800
Db GGTGACTACACTTGTGCCACTTAGAGCAAGACATATATGACAAAGTGTGTCTTGAGG 2642
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db TACAGGGCTCTCTCGGCATTTGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGCC 2702
821 LeuThrIleGlnValLeuThrValGlyAenAlaLeuArgProLysLysLysTyrThrTyr 840
Db TTGACCATCCAGGTCTTACTGTGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC 2762
841 PheValLysLysLysLysGluSerPheAenAlaIleProThrPheSerAlaTrpValIle 860
Db TTCGTAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2822
861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db GAAGAGTGGGGCAATGTTCTAAGTCACTGTGAATGGGTGGCAGAGAAGACTGGTAGAA 2882
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db TGCCGAGACATTAATGAGACAGCTGTCTCCAGTGTGCAAGAAAGTGAAGCAGCAGC 2942
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyLysTrpSerCys 920
Db ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCACTATG 3002
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisaspGly 940
Db TCTAAGACCTGTGGGAAGGTTTACAAAAAAGAAAGCTTCAAGTGTCTGTCCTCATGGA 3062
941 GlyValLeuSerHisaspSerCysAspProLeuLysLysProLysHisPheIleaspPhe 960
Db GGGGTGTATCATGAGAGCTGTGATCTCTTAAAGAAACCTTAACATTTTCATAGACTTT 3122
961 CysThrMetAlaGluCysSer 967
Db TGCACATGGCAGATGCAGT 3143

RESULT 10

US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308
Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.88% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 17 Gaps: 0
US-09-373-658c-126 (1-967) x US-10-159-563-308 (1-4459)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAen 20
Db 243 ATGCAGCAGCTGTGCCGAGGGTTCGGAAGCCCAAGCTGGCAGCGACATGGGGAC 302
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 303 GCGAGCGGGCTCCGGGGTCTCGAGCTTGGGCCGTACCCACCGCTGCTGCTCGCC 362
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 363 GCGGCGCTACTGGCGGTGTGCGACGACTCGGGGCGCCCTCCGAGGAGCAGGAGCTA 422
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 423 GTGGTCCCGAGCTGGAGCGGCCCGGACACAGGACCCAGCGCTCCGCTGCACGCC 482
QY 81 PheAspGlnGlnLeuAspLeuValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACAGCAGCTGATCTGGAGCTGGCGCCCGCAGCAGCAGCTTTTGGCGCCGGCTTC 542
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACGCTCCAGAACTGGGGCGAAATCCGGGTCCGAGACCGCGCTTCGGAACACCGACCTG 602
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 603 GCGCACTGCTTCTACTCCGGCACCGTGAATGCGATCCAGCTCGGCTCGGCCCTTCAGC 662
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 663 CTCCTCGAGGGCGTGGCGCGCCCTTCTACCTGCTGGGGAGCGCTATTTTCATCCAGCG 722
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 723 CTGCGCGCGCCAGCAGCGCTCGCCACCGCGCCCGCCAGGAGGAGGAGCGCGCGACCA 782
QY 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 783 CTACAGTTCCACTCTCTCGCGCGGAATCGGACGGGCGACGTCGCGGCGACGTCGGGGTC 842


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Db 3003 TCTAAGACCTGTGGGAAGGCTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 3062
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheLeuLeuAspPhe 960
Db 3063 GGGGTGTATCTCATGAGAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3122
Qy 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACATGGCAGATGCAGT 3143

RESULT 11
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Alignment Scores:
Pred. No.: 0 Length: 4760
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 10 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-971-429B-17 (1-4760)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 561 ATGCAGCAGCTGTGCCCGAGGGGTTCGAAAGCGCGAAGCTGGCGAGCAGATGGGGAAAC 620
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 621 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCAGTACCCACGCTGCTGCTCGCC 680
Qy 41 AlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 681 GCGGCGCTACTGCGCGCTGTCCGACGCACTCCGGCGCCCCCTCCGAGGAGCAGGAGCTA 740
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 741 GTGGTGCAGAGCTGAGCGCCCGCGGACACGGGACCCACGCGCTCCGCGCTGCACGCC 800
Qy 81 PheAspGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 801 TTTGACCAGCAGCTGGATCTGGAGCTGGCGGCCGACAGAGCTTTTGGCGCCCGGCTTC 860
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 861 ACCTCCAGACGTGGGGGCGAAATCCGGGTCCGAGACGCGCGCTTCGCGAAACCGACCTG 920

121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
921 GGCACACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCGCCCTCAGC 980
141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro 160
981 CTCCTCGAGGGCGTCCGCGGCGCTTCTACCTGCTGGGGAGGCGTATTTCATCCAGCGG 1040
161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
1041 CTGCCCCGCGCAGCAGCGCTCCGCCACCGCGCGCCAGGGGAGAACCGCGCGCACCA 1100
181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
1101 CTACAGTTCCACCTCTCTCGGGCGGAATCGGCAGGCGGAGCTAGGCGGACGCTGCGGGGTC 1160
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
1161 GTGGACGACGAGCCCGCGCGACTCGGAAAGCGGAGACCGAAGACGAGGACGAAGGACT 1220
221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
1221 GAGGCGGAGGACGAAAGGGGCTCAGTGGTGGCGCAGGACCCGCGCAGCTGCAAGCGCTAGGA 1280
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
1281 CAGCCCCACAGGACTGGAGAGCATTAAGAAAGAACGATTTGTGTCCAGTCCACGCTATGTG 1340
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
1341 GAAACCATGCTTGTGGCAGACCCAGTCGATGGCAGAAATCCACGGCAGTGGTCTAAAGCAT 1400
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
1401 TACCTTCTCACGTGTGTTTTTCGGTGGCAGCAGATGTACAAACACCCAGCAGCATTCGTAT 1460
301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
1461 TCAGTTAGCTTGGTGGTGGTGNAGATCTTGGTCATCCAGATGAACAGAGGGGCGGNA 1520
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
1521 GTGACCTCCATGCTGCTCCTCCTCTCGGGAACCTTTGCAACTGGCAGAGCAGCACAAC 1580
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
1581 CCACCCAGTGACCCGGGATGCGAGAGCATTATGACACAGCAATTCCTTTCCACGAGAGGAC 1640
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
1641 TTGTGTGGTCCAGACATGTGATCTTTGGGATGGCTGATGTGGAACTGTGTGTGAT 1700
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
1701 CCGAGCAGAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTGCCTTCCACACAGCC 1760
401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAspLeu 420
1761 CATGAATTAGCCACGCTGTTTAAACATGCCCATGATGATGCAAGAGAGTGTGCCAGCTTT 1820
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1821 AATGTTGTGAACACGAGATTTCCACATGATGGCTCAATGCTTTCCAACTGGACCCACAGC 1880
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1881 CAGCTTGTGCTCTCTTCGTGCTGCTTACATGATGATGATGATGATGATGATGATGATGATG 1940
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1941 GAATGTTTGTATGGACAGCCTCAGAAATCCATACAGCTCCCGAGGCGATCTCCCTGGCACC 2000
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
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Db	642	GTGTTGCGGAGCTGGAGCGCGCCCGGGGACACGGRGACCAACGCGCCTCTCGCCTTCGACGCC	701
Qy	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
Db	702	TTTGACGACGAGCTGGATCTGGAGCTCGGCCCGGCACAGCAGCTTTTGGCGCCCGGCTTC	761
Qy	101	ThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGluThrAspLeu	120
Db	762	ACGCTCCAGAACGTTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGCGAAACCGACCTG	821
Qy	121	AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
Db	822	CGGCACCTGCTTCTACTCCGGCACCGTGAATGGCGATCCCACTCGGCTGGCGCCTCAGC	881
Qy	141	LeuCysGluGlyValArgGlyValaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro	160
Db	882	CTCTGCGAGGGCGTGGCGGCGCTTCTACTGCTGGGGAGGCGTATTTCATCCAGCGC	941
Qy	161	LeuProAlaIaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro	180
Db	942	CTGCCCGCGCAGCGAGCGCTCGCACCGCGCCCGAGGGAGAAAGCGCGCGACCA	1001
Qy	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal	200
Db	1002	CTACAGTTCCACCTCTCTCGGCGGAAATCGGCAGGGCAGCTMGCGCGCACGTGCGGGGT	1061
Qy	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr	220
Db	1062	GTGACGACGAGCCCGCGCGACTGGGNAAGCGAGACCGNAGACGAGGACGAAAGGACT	1121
Qy	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
Db	1122	GAGGCGGAGGACGAAGGSGCTCAGTGTGCGCGCAGGACCCCGCACCTGCAAGGCGTAGGA	1181
Qy	241	GlnProThrGlyThrGlySerIleArgIlyLysArgPheValSerSerHisArgTyrVal	260
Db	1182	CAGCCCAACAGGAATCGGAAGCATAGAAGAAAGAGCATTTGTGTCCAGTCAACCGCTATGTG	1241
Qy	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
Db	1242	GAACACCATGTTGTGGCGACACGTCGATGGCAGAAATCCACGGCAGTGGTCTTAAACAT	1301
Qy	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
Db	1302	TACCTTCTCAGTTGTTTTCGTTGGCAGCCAGATTGTGTACAAACACCCCGCATTCGTAAT	1361
Qy	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
Db	1362	TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCAATCCACGATGAACAGAGGGCGGAA	1421
Qy	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
Db	1422	GTGACCTTCCAAATGTGCGCTTCTCGGAACTTTTGCAACTGGCAGAGCAGCACAC	1481
Qy	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
Db	1482	CCACCCAGTGACCGGGATGCAGACACTATGACACAGCAATCTCTTTCCACGACAGGAC	1541
Qy	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
Db	1542	TTGTGTGGGTCCCCAGACATGTGATCTTTGGGATGGCTGATGTTGGAACTGTGTGTGAT	1601
Qy	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400
Db	1602	CCGAGCAGAGAGCTGCTCGCTCATAGAGATGATGGTTTACAAAGCTGCTTCCACACAGCC	1661
Qy	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
Db	1662	CATGAATTAGGCCACGTTGTTAAATGCCACATGATGATGCNAAGCAGTGTGCCAGCTT	1721
Qy	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
Db	1722	AATGGTGTGAACACGAGATCCCATGATGGCGTCAATGCTTTTCCAACCTGGACACAGC	1781

Qy	441	GlnProThrSpSerProCysSerGlyTywEilleThrSerPheLeuAspAsnGlyHisGly	450
Db	1782	CAGCCTTTGGTCTCTCTCGCAGTGCCATCATGATTACATCATTTCTGGGATAATGTGTCATGGG	1841
Qy	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
Db	1842	GAATGTTTGATGNCACAGCTTCAGATCCCATACAGCTCCACAGCGNATCTCCCTGGCACC	1901
Qy	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerIysHisCysPro	500
Db	1902	TCGTACGATGCAACCCGGCAGTGCAGTTTACATATTTGGGAGGAGACTCCAAACACTGCCTCC	1961
Qy	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
Db	1962	GATGACCCAGCACATGTAGACCTTGTGTGTATCCGCGACCTCTGTGTGGGTGCTGGTG	2021
Qy	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
Db	2022	TGTCAAAACCAACACTTCCCTGGCGGATGGCACAGCTGTGGAGAAGGAAATGGTGT	2081
Qy	541	IleAsnGlyLysCysValAsnLysAsnHisArgIysHisPheAspThrPropheHisGly	560
Db	2082	ATCAACCGCCAAAGTGTGTGAACAAACACGACAGAAAGCATTTTATACGCTCTTTTCATGGA	2141
Qy	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln	580
Db	2142	AGCTGGGGGATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTGCRCTGGAGAGTCCAG	2201
Qy	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly	600
Db	2202	TACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGAGAGGGAAGTACTGTGAAGGC	2261
Qy	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
Db	2262	AAACGAGTGGCTACAGATCCTGTAACTTTGAGAGCTGTCCAGACAAATATGGAAAACC	2321
Qy	621	PheArgGluGlnCysGluAlaHisAsnGlnPheSerLysAlaSerPheGlySerGly	640
Db	2322	TTTATAGAGAGAACAAATGTGAAGCACACAACGAGTCTTCAAAAGCTTCTTTGGGAGTGGG	2381
Qy	641	ProAlaValGlnTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
Db	2382	CCTCGGTGGAATGGAATTCACAAAGTACGTGGCGGTCTCACAAAGGACAGGTGCACAGCTC	2441
Qy	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly	680
Db	2442	ATCTGCCAACCCAAAGGCATTTGGCTACTTCTTCTGTTTGCAGCCCAAGGTTGTAGATGGT	2501
Qy	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
Db	2502	ACTCCATGTAGCCCAAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAGCTGGT	2561
Qy	701	CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn	720
Db	2562	TGTGATCGCATCATAGACTCCAAAGAAGAGTTGATTAATGTGTGTTTCCGGGGGGAAT	2621
Qy	721	GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp	740
Db	2622	GGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTCAAAACCTGGATATCATGAT	2681
Qy	741	IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnArgGly	760
Db	2682	ATCATCAAAATCCAACTGGAGGCCACCAATCGAAGTGAAACAGCGGGAACCCAGAGGGGA	2741
Qy	761	SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn	780
Db	2742	TCCAGGAAACAATGGCAGCTTCTTGCCATCAAGCTGCTGATGSCACATATATCTTAAT	2801
Qy	781	GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg	800
Db	2802	GGTGNCATCACTTTGTCCACTTAGAGCAGACATATGTACAAAGGTGTGTCTTGAGG	2861

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Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2862 TACAGCGGCTCCTCTCGGCAATTTGGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGAGCCC 2921
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysIleThrTyr 840
Db 2922 TTGACCATCCAGGTCTTACTGTGGGCAATGCTTCCGACCTAAATTAATACACTAC 2981
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2982 TTCTGTAAGAAGAGAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 3041
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3042 GAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGGTGGGAGAGAGACTGGTAGAA 3101
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3102 TGCCGAGACATTAATGACAGCCTGCTTCCGAGTGTGCAAAAGCAAGTGAAGCCAGCCAGC 3161
Qy 901 ThrArgProCysAlaAlaPheHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3162 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGGAGCTGGTGCATCATGT 3221
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3222 TCTAAGACCTGTGGGAAGGGTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 3281
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3282 GGGGTGTATCTCATGAGAGCTGTGATCCCTTAAAGAAACCTTAAACATTTTCATAGACTTT 3341
Qy 961 CysThrMetAlaGluCysSer 967
Db 3342 TGCACAATGGCAGAATGCAGT 3362
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RESULT 13

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US-10-741-600-777
; Sequence 777, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4459)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-777
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Alignment Scores:

Pred. No.:	0	Length:	4459
Score:	5202.00	Matches:	953
Percent Similarity:	98.97%	Conservative:	4
Best Local Similarity:	98.55%	Mismatches:	10
Query Match:	98.39%	Indels:	0
DB:	19	Gaps:	0

US-09-373-658C-126 (1-967) x US-10-741-600-777 (1-4459)

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Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuLysSerAspMetGlyAsn 20
Db 243 ATGCAGCAGCTGTGCCCCGAGGGTTCCGAAGGCGCAAGCTGGGCGAGCATGGGGAAC 302
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Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db 303 GCGAGCGGCTCCGGGGTCTCGAGCTTTGGGCGMGTACCCACGCTGTGTCTGTCTCGCC 362
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerClnuAspGluGluLeu 60
Db 363 GGGGCGCTACTCGGCGGTGTTCGACGCACTCGGGCGCCCTTCGAGGAGGACGAGGAGCTA 422
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 423 GTGGTCCCGAGCTGGAGCGCGCCCGGACACGACGACCGCCCTCCGCTGCACGCC 482
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACCAGCAGCTGGATCTGGAGCTCGCGCCCGACAGCAGCTTTTGGCGCCCGGCTTC 542
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACCTCTCAAGACGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGAAACCGACCTG 602
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 603 GCGCATCTGTTCTACTCCGACCGCTGAATGGGATCCAGCTCGGCTCGGCTCGCCCTCAGC 662
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 663 CTCTGCGAGGCGTGGCGGCGCTTCTACTCTGGGGGAGGCGTATTTTCATCCAGCCG 722
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 723 CTGCCCGCGCCACGAGCGCTTCCGCCCGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 783 CTACAGTTTCCACCTCTCTGCGCGGAATCGCAGGGGAGCGCTMGCGGCGCACGTGCGGGGTS 842
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 843 GTGGACGAGCGAGCCCCCGCGCGCTGGGAAAGCGGAGACCGAAAGACGAGGAGGAGGAGG 902
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 903 GAGGCGGAGACGAGGAGGCTCAGTGTGTCCCGCAGGACCCCGGCTGCAAGGCGTATGGA 962
Qy 241 GlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHisArgTyrVal 260
Db 963 CAGCCACAGAACTGGAAGCATAAAGAAAGAGCGATTTGTTCAGTCCCGCTATGTG 1022
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1023 GAAACCATGCTTGTGGCAGACCATGATGGCAGAAATTCACGCGCAGTGGTCTAAAGCAT 1082
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1083 TACCTTCTCAGTGTGTTTTCGTTGGCAGCCAGATTTGACAAACACCCCGCATTTCTGTAAT 1142
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1143 TCAGTTAGCTGTGGTGGTGAAGATCTTGTGTATCCACGATGAACAGAGGCGCGGAA 1202
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
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Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1263 CCACCCAGTACCAGGATGCAGACACTATGACACAGCAATTTCTTTTCCACAGACAGGAC 1322
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1323 TTGTGTGGTCCCCAGACATGTGATCTTGGGATGGCTGTGTTGGTGGTGTGTGTGT 1382
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
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1383 DB CCGAGCAGAAAGCTGCTCCGCTCAGTAGAAGATGATGGTTTACAAAGCTGCCCTTACCACAGCC 1442
401 QY HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
1443 DB CATGAATTAGGCCACGCTGTTTAACTAGCCACATGATGATGCAAGCAGGTGTCAGACCTT 1502
421 QY AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1503 DB ANTGGTGTGACACAGGATTTCCACATGATGGGTCAATGCTTTCCAACTGGACACAGC 1562
441 QY GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1563 DB CAGCCTTGCTCCTTGGCAGTGCTACATGATTTACATCATTTCTGGATAATGGTCATGGG 1622
461 QY GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1623 DB GAATGTTTGTATGACAAAGCTCAGATCCCATACAGCTCCAGGGGATCTCCCTGGCACC 1682
481 QY SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1683 DB TGTACGATGCCAACCGGAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1742
501 QY AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
1743 DB GATGCAGCCAGCACATGTAGCACTTGTGTGTACCGGCACCTCTGGTGGGTGCTGGTG 1802
521 QY CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
1803 DB TGTCAACCAAAACACTTCCCGTGGGGATGGCAGCCAGCTGTGGAGAGGAAATGGTGT 1862
541 QY IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
1863 DB ATCAACGGCAAGTGTGTGAACAAACCCGACAAAGACATTTTGATACGCCCTTTTATGGA 1922
561 QY SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
1923 DB AGCTGGGAATGTGGGGCTTGGGGAGACTGTTCGAGAACGTGCGRTGGAGAGTCCAG 1982
581 QY TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
1983 DB TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC 2042
601 QY LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
2043 DB AAACGAGTGGCTACAGATCTGTACCTTGAGGACTGTCCAGACAAATATGAAAAACC 2102
621 QY PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
2103 DB TTTAGAGAGGAACAATGTGAAGCACACACAGAGTTTCAAAAGCTTCCCTTGGGAGTGG 2162
641 QY ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2163 DB CTTGGGTGGAATGGATTTCCAAAGTACGTGGCGTCTCAACCAAGACAGGTGCAAGCTC 2222
661 QY IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2223 DB ATCTGCCAGCCAAAGGCAATGGCTACTTCTTCGTTTTCAGCCCAAGTTTGTAGTGT 2282
681 QY ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
2283 DB ACTCCATGTAGCCAGATTTCCACCTCTGCTGTGTGCAAGGACAGTGTGTAAGACTGGT 2342
701 QY CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2343 DB TGTGATCGCATCATGACTCCAAAAAGAAAGTTGATAAATGTGGTGTGGGGGGAAT 2402
721 QY GlySerThrCysLysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2403 DB GGATCTACTTGTAAAAAATAATACAGATCAGTACTAGTGTGCAAAACCTGGATATCATAT 2462
741 QY IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760

2463 DB ATCATCACAATTTCCAACTGGAGCCCAACCACTGAAGTGAACAGCGGAAACAGAGGGA 2522
761 QY SerArgAsnAsnGlySerPheLeuAlaIleLysAlaIleAspGlyThrTyrIleLeuAsn 780
2523 DB TCCAGGAACAATGGCAGCTTTCTTCCCATCAAGCTGCTGATGGCACAATATATCTTAAT 2582
781 QY GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2583 DB GGTGNTACTACATTTGTCCACCTTAGAGCAGACATATGTACAAAGGTGTGTCTTGAGG 2642
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2703 DB TTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAAATACACCTAC 2762
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2763 DB TTCGTAAGAGAGAGAGAGATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 2822
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2883 DB TCCGAGACATTAATGGAGCAGCTGCTTCCGAGTGTGCAAGGAAGTGAAGCAGCCAGC 2942
901 QY ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerCys 920
2943 DB ACCAGACTTGTGACAGCATCCCTGCCCCAGTGGGAGTGGGTCAATCATGT 3002
921 QY SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
3003 DB TCTAAGACTGTGGGAAGGGTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATATGGA 3062
941 QY GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
3063 DB GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATGACTTT 3122
961 QY CysThrMetAlaGluCysSer 967
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US-10-741-600-775
; Sequence 775, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 4658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4658)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-741-600-775
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Pred. No.: 0 Length: 4658
Score: 5202.00 Matches: 953
Percent Similarity: 98.97% Conservative: 4

Best Local Similarity: 98.55%				Matches: 10			
Query Match: 98.39%				Indels: 0			
DB: 19				Gaps: 0			
US-09-373-658C-126 (1-967) x US-10-741-600-775 (1-4658)							
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QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40	QY	361	LeuGlyGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	522	GCGAGCGGGCTCCGGGCTCTCGAGCTTGGCGCGTATCCACCGCTGCTGCTGCC	581	DB	1542	TTGTGTGGGTCCACAGCATGTATCTTGGATGGCTGATGTTGGAACCTGTGTGTGAT	1601
QY	41	AlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu	60	QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla	400
DB	582	GCGGCGCTACTGGCGCTGTCGAGCGACTCGGGCGCCCTCCGAGGAGGACGAGGACTA	641	DB	1602	CCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGCTGCCCTTCCACACAGCC	1661
QY	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla	80	QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
DB	642	GTGTGCGGAGCTGGAGCGCGCCCGGACACRGCACCGCCCTCCGCTCGCACGCC	701	DB	1662	CATGAATTAGGCCACGTTTTAATCATGCCACATGATGATGCAAGCAGGTGTGCCAGCTT	1721
QY	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100	QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	702	TTTGACCCAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGCGCCCGCTTC	761	DB	1722	AATGGTGTGAACAGGATTTCCACATGATGGGTCAATGCTTTCCAACTGGACACAGC	1781
QY	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu	120	QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	762	ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGGAACCGACCTG	821	DB	1782	CAGCCTTGCTCTCTTGCAGTGCCTACATGATTACATCATTTCTGGATAATGTCATGGG	1841
QY	121	AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140	QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	822	GCGCACTGCTTACTCCGCGCACCGTGAATGGCGATCCACAGCTCGGCTCGCGCCCTCAGC	881	DB	1842	GAATGTTTATGGACCAAGCTCAGATCCCATACAGTCCCGAGCGCATCTCCCTGGCAC	1901
QY	141	LeuGlyGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheIleGlnPro	160	QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	882	CTCTGGAGGCGGTGGCGCGCTTCTACCTGCTGGGGAGCGGTATTTCATCCAGCGG	941	DB	1902	TGCTAGCATGCCAACCGCGCAGTCCAGTTCATATTTGGGGAGGACTCCAAACACTGCCCY	1961
QY	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro	180	QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	942	CTGCCCGCCGACGAGCGCTCGCACCGCCGCCCGCCGAGGAGGAGCGCGGACCA	1001	DB	1962	GATGCAGCCAGCACATGTAGCACTTGTGTGTACCGGCACCTCTGTGGGTGCTGGTG	2021
QY	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal	200	QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	1002	CTACAGTTCCACCTCTCGCGCGGAATCGCAGCGGCGCAGCTGCGGCGCACGTGCGGGTS	1061	DB	2022	TGTCAAACCAACACTCCCGTGGCGGATGGCACCGTGTGGAGAGGGAATGGTGT	2081
QY	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGlyThr	220	QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	1062	GTGGACGACGAGCCCCCGCGCTGAGTGGGAAAGCGGAGACCGAAGACGAGGAGGACT	1121	DB	2082	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATAGCCTTTTCATGGA	2141
QY	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240	QY	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	1122	GAGGGCGAGGACGAGGSGCTCAGTGTGCTCCCGCAGGACCCCGCATGCAAGCGTAGGA	1181	DB	2142	AGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTTCGAGAAAGCTGTCGTGGAGGATCCAG	2201
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QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLysHis	280	QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
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QY	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320	QY	641	ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
DB	1362	TCAGTAGCTGTGTGTGTGAAGATCTTGTTCATCCAGTGAACAGAGGCGCGGAA	1421	DB	2382	CCTGCGGTGGAATGGATTTCCAAAGTACGCTGGCGTCTCCACCAAGGAGCAGGTGCAAGCTC	2441
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340	QY	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly	680
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QY	341	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700	QY	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
DB	1481	GTGACCTTCAATGTCGCCCTCACTCTCGGAACTTTTTCGCAACTGGCAGAGCAGTGTGTAAAGCTGGT	2561	DB	2502	ACTCCATGTATGCCAGATTCCACTCTGTCTGTGTGCAAGGACAGTGTGTAAAGCTGGT	2561

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; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
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; LOCATION: (1)..(2853)
; NAME/KEY: UNSURE
; LOCATION: (3095)
; OTHER INFORMATION: May be any nucleic acid
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; OTHER INFORMATION: May be any nucleic acid
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; LOCATION: (3255)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3261)
; OTHER INFORMATION: May be any nucleic acid
US-09-373-658-1
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Score: 5144.00 Matches: 940
Percent Similarity: 99.37% Conservative: 4
Best Local Similarity: 98.95% Mismatches: 6
Query Match: 97.30% Indels: 0
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DB 121 GAGGAGCTAGTGTCTCCGAGCTGGAGCGCGCCCGGACACGCGACCGCCGCTCCGC 180
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